

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 18:38:23 ; Search time 18 Seconds
(without alignments)

1220.756 Million cell updates/sec

Title: US-10-040-884-3

Perfect score: 2192

Sequence: 1 MGMTMLLECSLSKLCVIO.....LYAAVAGIRVESLFYNYSM 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446.5	20.4	806	1	CEK2_CHICK
2	444	20.3	801	1	FGK3_MOUSE
3	444	20.3	806	1	FGK3_MOUSE
4	434	19.8	802	1	FGK4_HUMAN
5	433	19.8	821	1	FGK2_MOUSE
6	428.5	19.5	822	1	FGK1_MOUSE
7	427.5	19.5	808	1	FGK4_MOUSE
8	427	19.5	821	1	FGK2_HUMAN
9	424	19.3	822	1	FGK1_HUMAN
10	424	19.3	822	1	ABL1_MOUSE
11	419	19.1	746	1	ABL1_MOUSE
12	419	19.1	1123	1	ABL1_MOUSE
13	417	19.0	1130	1	ABL1_HUMAN
14	416	19.0	812	1	ABL1_XENLA
15	415	18.9	822	1	FGK1_RAT
16	415	18.9	823	1	CEK3_CHICK
17	407.5	18.6	1182	1	ABL2_HUMAN
18	403.5	18.4	439	1	ABL1_FSVHY
19	397	18.1	813	1	FGK2_XENLA
20	391	17.8	1138	1	TIE1_HUMAN
21	390	17.8	1134	1	TIE1_MOUSE
22	388	17.7	729	1	FGK1_DROME
23	388	17.7	1136	1	TIE1_BOVIN
24	384	17.5	1520	1	ABL_DROME
25	382	17.4	773	1	CD96_DROME
26	379	17.3	506	1	SRK4_SPOLA
27	376.5	17.2	1052	1	FGK2_DROME
28	373	17.0	370	1	SEA_AVLET
29	370.5	16.9	825	1	TRKC_PIG
30	369	16.8	992	1	FLT3_MOUSE
31	368.5	16.8	1224	1	ABL1_CAEEL
32	367.5	16.8	778	1	TRKA_CHICK
33	366	16.7	1115	1	RET_MOUSE

34 365 16.7 1097 1 PGDR RAT
35 364 16.6 450 1 CSK_HUMAN
36 363.5 16.6 1040 1 EGI5_CAEEL
37 363.5 16.6 1087 1 PGDS_XENLA
38 362.5 16.5 993 1 FLT3_HUMAN
39 362 16.5 505 1 SRK1_SPOLA
40 362 16.5 1378 1 RON_MOUSE
41 361.5 16.5 450 1 CSK_RAT
42 361 16.5 786 1 RTKL_DROME
43 360.5 16.4 1125 1 TIE2_BOVIN
44 360 16.4 362 1 SRK2_SPOLA
45 360 16.4 1098 1 PGDR_MOUSE

ALIGNMENTS

RESULT 1
CEK2_CHICK STANDARD; PRT; 806 AA.
AC P18460;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine kinase receptor CEK2 precursor (EC 2.7.1.112).
GN CEK2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90332672; PubMed=2165604;
RA Pasquale E.B.;
RT "A distinctive family of embryonic protein-tyrosine kinase
receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5812-5816(1990).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
EMBL; M35195; AAA48664.1; -
PIR; A35963; A35963.
DR HSSP; P11362; 1FGK.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;

RA Superti-Furga A., Eich G., Bucher H.U., Wisser J., Giedion A.,
 RA Gitzelmann R., Steinmann B.;
 RT "A glycine 375-to-cysteine substitution in the transmembrane domain
 RT of the fibroblast growth factor receptor-3 in a newborn with
 RT achondroplasia.";
 RL Eur. J. Pediatr. 154:215-219(1995).
 RN [10]
 RP VARIANT TD1 CYS-249.
 RX MEDLINE=96154693; PubMed=8589699;
 RA Tavormina P.L., Rimoin D.L., Cohn D.H., Zhu Y.-Z., Shiang R.,
 RA Wasmuth J.J.;
 RT "Another mutation that results in the substitution of an unpaired
 RT cysteine residue in the extracellular domain of FGFR3 in
 RT thanatophoric dysplasia type I.";
 RL Hum. Mol. Genet. 4:2175-2177(1995).
 RN [11]
 RP VARIANTS TD1 CYS-248 AND CYS-371, AND VARIANT TD2 GLU-650.
 RX MEDLINE=95291326; PubMed=7773297;
 RA Tavormina P.L., Shiang R., Thompson L.M., Zhu Y.-Z., Wilkin D.J.,
 RA Lachman R.S., Wilcox W.R., Rimoin D.L., Cohn D.H., Wasmuth J.J.;
 RT "Thanatophoric dysplasia (types I and II) caused by distinct
 RT mutations in fibroblast growth factor receptor 3.";
 RL Nat. Genet. 9:321-328(1995).
 RN [12]
 RP VARIANT HYPOCHONDROPLASIA LYS-540.
 RX MEDLINE=95400307; PubMed=7670477;
 RA Bellus G.A., McIntosh I., Smith E.A., Avlsworth A.S., Kaitila I.,
 RA Horton W.A., Greenhaw G.A., Hecht J.T., Francomano C.A.;
 RT "A recurrent mutation in the tyrosine kinase domain of fibroblast
 RT growth factor receptor 3 causes hypochondroplasia.";
 RL Nat. Genet. 10:357-359(1995).
 RN [13]
 RP VARIANT CROUZON GLU-391.
 RX MEDLINE=96083601; PubMed=7493034;
 RA Meyers G.A., Orlow S.J., Munro I.R., Przybyla K.A., Jabs E.W.;
 RT "Fibroblast growth factor receptor 3 (FGFR3) transmembrane mutation
 RT in Crouzon syndrome with acanthosis nigricans.";
 RL Nat. Genet. 11:462-464(1995).
 RN [14]
 RP CHARACTERIZATION OF VARIANT ARG-380.
 RX MEDLINE=96174812; PubMed=8599935;
 RA Webster M.K., Donoghue D.J.;
 RT "Constitutive activation of fibroblast growth factor receptor 3 by
 RT the transmembrane domain point mutation found in achondroplasia.";
 RL EMBO J. 15:520-527(1996).
 RN [15]
 RP VARIANTS TD1 CYS-248, CYS-249, CYS-370 AND CYS-373.
 RX MEDLINE=96254981; PubMed=8845844;
 RA Rousseau F., el Ghoulzi V., Delezoide A.L., Legeai-Mallet L.,
 RA le Merrer M., Munnich A., Bonaventure J.;
 RT "Missense FGFR3 mutations create cysteine residues in thanatophoric
 RT dwarfism type I (TD1).";
 RL Hum. Mol. Genet. 5:509-512(1996).
 RN [16]
 RP VARIANT CRS3 ARG-250.
 RX MEDLINE=97195541; PubMed=9042914;
 RA Muenke M., Gripp K.W., McDonald-McGinn D.M., Gaudenz K.,
 RA Whitaker L.A., Bartlett S.P., Markowitz R.I., Robin N.H., Nwokoro N.,
 RA Mulvihill J.J., Losken H.W., Mulliken J.B., Guttmacher A.E.,
 RA Wilroy R.S., Clarke L.A., Holloway G., Ades L.C., Haan E.A.,
 RA Mulley J.C., Cohen M.M., Bellus G.A., Francomano C.A.,
 RA Moloney D.M., Wall S.A., Wilkie A.O.M., Zackai E.H.;
 RT "A unique point mutation in the fibroblast growth factor receptor 3
 RT gene (FGFR3) defines a new craniosynostosis syndrome.";
 RL Am. J. Hum. Genet. 60:555-564(1997).
 RN [17]
 RP VARIANT TD1 CYS-370.
 RX MEDLINE=99004917; PubMed=9790257;
 RA Katsumata N., Kuno T., Miyazaki S., Mikami S., Nagashima-Miyokawa A.,
 RA Kimura A., Horikawa R., Tanaka T.;
 RT "G370C mutation in the FGFR3 gene in a Japanese patient with
 RT thanatophoric dysplasia.";
 RL Endocr. J. 45:S171-S174(1998).

RN [18]
 RP VARIANT HYPOCHONDROPLASIA VAL-538.
 RA Grigelloni G., Hagenaes L., Ekloef O., Neumeyer L., Haerleid P.E.,
 RA Anvret M.;
 RT "A novel missense mutation Ile538Val in the fibroblast growth
 RT factor receptor 3 in hypochondroplasia.";
 RL Hum. Mutat. 11:333-333(1998).
 RN [19]
 RP VARIANT HYPOCHONDROPLASIA THR-540.
 RX MEDLINE=98112422; PubMed=9452043;
 RA Deutz-Terlouw P.P., Losekoot M., Aalfs C.M., Hennekam R.C.M.,
 RA Bakker E.;
 RT "Asn540Thr substitution in the fibroblast growth factor receptor 3
 RT tyrosine kinase domain causing hypochondroplasia.";
 RL Hum. Mutat. Suppl. 1:S62-S65(1998).
 RN [20]
 RP VARIANT TD1 MET-650.
 RA Kitch H., Brodie S.G., Kupke K.G., Lachman R.S., Wilcox W.R.;
 RT "Lys650Met substitution in the tyrosine kinase domain of the
 RT fibroblast growth factor receptor gene causes thanatophoric dysplasia
 RT type I.";
 RL Hum. Mutat. 12:362-363(1998).
 RN [21]
 RP VARIANTS BLADDER AND CERVIX CANCERS CYS-248; CYS-249; CYS-370 AND
 RP GLU-650.
 RX MEDLINE=99400545; PubMed=10471491;
 RA Cappellen D., De Oliveira C., Ricot D., Gil Diez de Medina S.,
 RA Bourdin J., Sastre-Garau X., Chopin D., Thierry J.P., Radvanyi F.;
 RT "Frequent activating mutations of FGFR3 in human bladder and cervix
 RT carcinomas.";
 RL Nat. Genet. 23:18-20(1999).
 CC -!- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.
 CC -!- PREFERENTIALLY BINDS FGF1.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=I1ic;
 CC IsoId=P22607-1; Sequence=Displayed;
 CC Name=2; Synonyms=I1Ib;
 CC IsoId=P22607-2; Sequence=VSP_002988;
 CC Name=3;
 CC IsoId=P22607-3; Sequence=VSP_002989;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, KIDNEY AND TESTIS. VERY
 CC LOW OR NO EXPRESSION IN SPLEEN, HEART, AND MUSCLE. IN 20- TO 22-
 CC WEEK OLD FETUSES IT IS EXPRESSED AT HIGH LEVEL IN KIDNEY, LUNG,
 CC SMALL INTESTINE AND BRAIN, AND TO A LOWER DEGREE IN SPLEEN, LIVER,
 CC AND MUSCLE. EPITHELIAL CELLS SHOW EXCLUSIVELY ISOFORM 2
 CC TRANSCRIPTS WHILE FIBROBLASTIC CELLS SHOW A MIXTURE OF ISOFORMS 1
 CC AND 2 TRANSCRIPTS.
 CC -!- DISEASE: Defects in FGFR3 are the cause of achondroplasia (ACH)
 CC [MIM:100800]. ACH is an autosomal dominant disease and is the most
 CC frequent form of short-limb dwarfism. It is characterized by a
 CC long, narrow trunk, short extremities, particularly in the

Query Match 20.3%; Score 444; DB 1; Length 806;
 Best Local Similarity 30.5%; Pred. No. 2e-26;
 Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;
 QY 34 VTIFILLGVILWLFIREQRTQQQRSGP---QGIAPVPPPPDLISWEAGHGNGVALPL-KE 89
 DB 381 VGFFLFVLVAAVTLCLRPSPKGLSPVTHKLSRFLKRVLSLENSASNTPLVRI 440
 QY 90 TSVENFLGATTPALAKIQVP-----REQLSVLEQICSGSCGPIFRANNTGDP 139
 DB 441 ARLSSGEGPTLVNVELEPADPKWLSRLTLGKPLGEGCFGVVMAEAIGDKORAA 500
 QY 140 KPKSVILKALKEPAGLHEVDFLGRIOFHQVLGHKNVLQLEGCTEKLPLYMWLEDAQ 199
 DB 501 KPTVAVKMLKDDATDKDLSLVSEMMKMIGHKHNIINLLGACTQGGPLYLVEYAAK 560
 QY 200 GDLLGLWTCRRDVTMTDGLLY-----DLTEKQVHVHIGKQVLLALEFLOEKHLFH 249

```

Db 561 GNLREFL-RARP-----PGLDYSFDTCKPEPBLQTLFQDLVSCAYQVARGMEYLSQKCIH 615
Qy 250 GDAARNILMQSLDTAKLGLGLGLAVYVYTRGAISSQT--IFLKLWAPERLLLRPASIRA 307
Db 616 RDLAARNLVATDNNYMKIADFGARDVHNLDDYKTKTNGRLFLVQWMAPEALFDRYVTHQS 675
Qy 308 DWFSFGILLYEMVTLCAPPYPPVPTSLILELQRRKMKRPPSSCTHTWYSIMKSCWRNRE 367
Db 676 DWFSFGVLLWEITLGGSPYGPGLVEELFKLKEGHRMDKPCANTCHDLIMWRECHHAAP 735
Qy 368 ADPSPRELRLLEAAIK-TADDE 390
Db 736 SQPTFKQLVDLDRVLVTSTDE 759

RESULT 4
FGR4 HUMAN
ID FGR4 HUMAN STANDARD; PRT; 802 AA.
AC P22455; O43785; Q14309;
DT 01-AUG-1991 (Rel. 19, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibroblast growth factor receptor 4 precursor (EC 2.7.1.112) (FGFR-4).
GN FGFR4 OR JTK2 OR TKF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID:9606;
RN [1]
RX SEQUENCE FROM N.A.
RA Partanen J.M., Mäkeläe T.P., Eerola E., Korhonen J., Hirvonen H.,
RA Claesson-Welsh L., Alitalo K.;
RT "FGFR-4, a novel acidic fibroblast growth factor receptor with a
RT distinct expression pattern.";
RL EMBO J. 10:1347-1354(1991).
RN [2]
RX SEQUENCE FROM N.A.
RA TISSUE=Mammary gland;
RX MEDLINE=93194827; PubMed=7680645;
RA Ron D., Reich R., Chedid M., Lengel C., Cohen O.E., Chan A.M.,
RA Neufeld G., Miki T., Tronick S.R.;
RT "Fibroblast growth factor receptor 4 is a high affinity receptor for
RT both acidic and basic fibroblast growth factor but not for
RT keratinocyte growth factor.";
RL J. Biol. Chem. 268:5388-5394(1993).
RN [3]
RX SEQUENCE FROM N.A.
RA MEDLINE=98119018; PubMed=9457674;
RA Kostezwa M., Muller U.;
RT "Genomic structure and complete sequence of the human FGFR4 gene.";
RL Mamm. Genome 9:131-135(1998).
RN [4]
RX SEQUENCE FROM N.A.
RA TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

```

```

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 609-676 FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=91062389; PubMed=2247464;
RA Partanen J., Mäkeläe T.P., Alitalo K., Leivaeslaihio H., Alitalo K.;
RT "Putative tyrosine kinases expressed in K-562 human leukemia cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).
CC -!- FUNCTION: RECEPTOR FOR ACIDIC FIBROBLAST GROWTH FACTOR. DOES NOT
CC BIND TO BASIC FIBROBLAST GROWTH FACTOR. BINDS FGFR19.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X57205; CAA40490.1; -
DR EMBL; L03840; AAB59389.1; -
DR EMBL; Y13901; CAA74200.1; -
DR EMBL; BC011847; AAH11847.1; -
DR EMBL; M59373; AA63208.1; -
DR FIR; S15345; TVRUF4.
DR PDB; 1QCT; 15-JUN-99.
DR Genew; HGNC:3691; FGFR4.
DR MIM; 134935; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005007; F:fibroblast growth factor receptor activity; TAS.
DR GO; GO:0008543; P:FGF receptor signaling pathway; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR007019; Prot kinase.
DR InterPro; IPR001245; Tyr kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR0109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
KW Repeat; Signal; Polymorphism; 3D-structure.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 802 FIBROBLAST GROWTH FACTOR RECEPTOR 4.
FT DOMAIN 25 369 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 370 390 POTENTIAL.
FT DOMAIN 391 802 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 30 128 IG-LIKE C2-TYPE 1.
FT DOMAIN 152 240 IG-LIKE C2-TYPE 2.
FT DOMAIN 249 349 IG-LIKE C2-TYPE 3.
FT DOMAIN 467 755 PROTEIN KINASE.
FT NP BIND 473 481 ATP (BY SIMILARITY).
FT BINDING 503 503 ATP (BY SIMILARITY).
FT ACT SITE 612 612 BY SIMILARITY.
FT MOD RES 643 643 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT DISULFID 57 101 POTENTIAL.
FT DISULFID 172 224 POTENTIAL.

```

FT DISULFID 271 333 POTENTIAL.
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 388 388 G -> R (in dbSNP:351855).
 FT CONFLICT 297 297 D -> V (IN REF. 1).
 FT SEQUENCE 802 AA; 87954 MW; B22B259831BB889F CRC64;
 Query Match 19.8%; Score 434; DB 1; Length 802;
 Best Local Similarity 29.8%; Pred. No. 1.2e-25;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;
 QY 21 EKQYEVLIV---PTLAVTIFLLGLVLLWLFIREQRTQQRSGP-----QGIAPVPPRDL 73
 Db 364 EARYTDLILVAGSLALAVLLLAGL-----YRQALHGRHPRPPATVQKLSRFFLARQF 418
 QY 74 SWEAGHGNNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-RQICSGSC 125
 Db 419 SLESGGSGKSSSLVGRVSSSGPALLAGLSLDLPDLWFFPRDLVGLKPLGEGCF 478
 QY 126 GPIFRAMNTGDSKP---KSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQLEG 182
 Db 479 GQVRAEAFGMDPARPDQASTAVKMLKONASDKDLADLVSEVMVKLIGRHKNIINLLG 538
 QY 183 CCKEKLPLYWLVEDVAGDGLGLFWTCRRDV-----MTMDG-----LLVDLTKQVYHIG 232
 Db 539 VCTQEGELVIVCAKGNLREFL-RARRPPGPDSPDGRPSSEGLSPFVLVSCAY--- 594
 QY 233 KQVLLALEFLQKHLPHGDVAARNILMQSLDTAKLGLGLAYEVYTRGAISSQT--IPL 290
 Db 595 -QVARGMQLSKRCIHRDLAARNVLVTEDNVWKIADFGLARGVHHIDYKYKTSNGLPV 653
 QY 291 KWLAPRILLRPAIRADVWVSFGILLIYEMVTLCAPYEPVPTTSILEHQRKIMKRPSS 350
 Db 654 KWMAPALPDVRYTHOSDVMVSFGILLWEITFLGSGSPYGPVPELFSLLREGRHMDRPPH 713
 QY 351 CTHMYTSIMKSWREADRPSPRELRLRLRLAAIKTADDE 390
 Db 714 CPPELYGLMRECHWAAPSQRPTFKQLVEALDKVLLAVSEE 753

RESULT 5

FGFR2_MOUSE
 ID_FGR2_MOUSE STANDARD; PRT; 821 AA.
 AC P21803; O55141; Q00389; Q61342;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibroblast growth factor receptor 2 precursor (EC 2.7.1.112) (FGFR-2)
 DE (Keratinocyte growth factor receptor).
 GN FGFR2 OR ECT1 OR BEK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=92228773; PubMed=1373495;
 RA Mansukhani A., Dell'Bra P., Moscatelli D., Kornbluth S.,
 RA Hanafusa H., Basilico C.;
 RT "Characterization of the murine BEK fibroblast growth factor (FGF)
 RT receptor: activation by three members of the FGF family and
 RT requirement for heparin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3305-3309(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=91270892; PubMed=1711190;
 RA Raz V., Keilman Z., Avioli A., Neufeld G., Givol D., Yarden Y.;

RT "PCR-based identification of new receptors: molecular cloning of a
 RT receptor for fibroblast growth factors.";
 RL Oncogene 6:753-760(1991).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=91095977; PubMed=1846048;
 RA Miki T., Fleming T.P., Bottaro D.P., Rubin J.S., Ron D.,
 RA Aaronson S.A.;
 RT "Expression cDNA cloning of the KGF receptor by creation of a
 RT transforming autoexon loop.";
 RL Science 251:72-75(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RX MEDLINE=98167854; PubMed=9499422;
 RA Twigg S.R.F., Burns H.D., Oldridge M., Heath J.K., Wilkie A.O.M.;
 RT "Conserved use of non-canonical 5' splice site (GA) in alternative
 RT splicing by fibroblast growth factor receptors 1, 2 and 3.";
 RL Hum. Mol. Genet. 7:685-691(1998).
 RN [5]
 RP SEQUENCE OF 477-821 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89219016; PubMed=2468939;
 RA Kornbluth S., Paulson K.E., Hanafusa H.;
 RT "Novel tyrosine kinase identified by phosphotyrosine antibody
 RT screening of cDNA libraries.";
 RL Mol. Cell. Biol. 8:5541-5544(1988).
 CC -!- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.
 CC POSSESSES A HIGHER AFFINITY FOR ACIDIC THAN FOR BASIC EGF'S.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P21803-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P21803-2; Sequence=VSP_002985, VSP_002986, VSP_002987;
 CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
 CC family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M86441; AAA37286.1; -;
 CC EMBL; X55441; CAA39083.1; -;
 CC EMBL; M63503; AAA39377.1; -;
 CC EMBL; Y16152; CAA76098.1; -;
 CC EMBL; Y16167; CAA76099.1; -;
 CC EMBL; M23362; AAA37285.1; -;
 CC PIR; A44142; TWMSBK.
 CC PIR; S17295; S17295.
 CC HSSP; P11362; 1FGK.
 CC MGD; MGI:95523; Fgfr2.
 CC GO; GO:0007435; P:salivary gland morphogenesis; IMP.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003598; Ig_c2.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR001245; Tyr_kinase.
 CC InterPro; IPR008266; Tyr_kinase_AS.
 CC Pfam; PF00047; ig; 3.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00408; Igc2; 3.
 CC SMART; SM00219; Tyrc; 1.
 CC PROSITE; PS50835; IG-LIKE; 3.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

RT genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8180-8184(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 17).
 RX MEDLINE=91274356; PubMed=1647213;
 RA Seno M., Sasada R., Watanabe T., Ishimaru K., Igarashi K.;
 RT "Two cDNAs encoding novel human FGF receptor.";
 RL Biochim. Biophys. Acta 1089:244-246(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Stomach cancer;
 RX MEDLINE=90332706; PubMed=2377625;
 RA Hattori Y., Odagiri H., Nakatani H., Miyagawa K., Naito K.,
 RA Sakamoto H., Katoh O., Yoshida T., Sugimura T., Terada M.;
 RT "K-sam, an amplified gene in stomach cancer, is a member of the
 RT heparin-binding growth factor receptor genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5983-5987(1990).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 5; 14 AND 15).
 RX MEDLINE=92212948; PubMed=1313574;
 RA Katoh M., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y.,
 RA Sugimura T., Terada M.;
 RT "K-sam gene encodes secreted as well as transmembrane receptor
 RT tyrosine kinase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2960-2964(1992).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Placenta;
 RX MEDLINE=93016048; PubMed=1400433;
 RA Dell K.R., Williams L.T.;
 RT "A novel form of fibroblast growth factor receptor 2. Alternative
 RT splicing of the third immunoglobulin-like domain confers ligand
 RT binding specificity.";
 RL J. Biol. Chem. 267:21225-21229(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 19), AND VARIANT ARG-613.
 RC TISSUE=Mammary gland;
 RX MEDLINE=92108030; PubMed=1309608;
 RA Miki T., Bottaro D.P., Fleming T.P., Smith C.L., Burgess W.H.,
 RA Chan A.M.-L., Aaronson S.A.;
 RT "Determination of ligand-binding specificity by alternative splicing:
 RT two distinct growth factor receptors encoded by a single gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:246-250(1992).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 19).
 RC TISSUE=Breast, and Cornea;
 RX MEDLINE=95170769; PubMed=7866434;
 RA Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch A.M.,
 RA Shay J.W.;
 RT "Hepatocyte growth factor (HGF), keratinocyte growth factor (KGF), and
 RT their receptors in human breast cells and tissues: alternative
 RT receptors.";
 RL Cell. Mol. Biol. Res. 40:337-350(1994).
 RN [9]
 RP ERRATUM.
 RC TISSUE=Breast, and Cornea;
 RA Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch A.M.,
 RA Shay J.W.;
 RL Cell. Mol. Biol. Res. 40:707-707(1994).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT CS SER-342.
 RC TISSUE=Blood;
 RA Steinberger D., Mueller U.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORMS 7; 9; 10; 11; 12 AND 13), AND VARIANT
 RP ARG-613.
 RX MEDLINE=20090220; PubMed=10626794;
 RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,
 RA Ishii H., Yanagihara K., Mafune K.-I., Makuuchi M., Terada M.;
 RT "Deletion of the carboxyl-terminal exons of K-sam/FGFR2 by short
 RT homology-mediated recombination, generating preferential expression
 RT of specific messenger RNAs.";
 RL Nat. Genet. 8:98-103(1994).
 RN [12]
 RP SEQUENCE FROM N.A. (ISOFORMS 5; 6; 8; 14 AND 18).
 RX MEDLINE=21845873; PubMed=11856867;
 RA Ingersoll R.G., Paznekas W.A., Tran A.K., Scott A.F., Jiang G.,
 RA Jabs E.W.;
 RT "Fibroblast growth factor receptor 2 (FGFR2): genomic sequence and
 RT variations.";
 RL Cytogenet. Cell Genet. 94:121-126(2001).
 RN [13]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Lind D.L., Cox D.R.;
 RT "Sequence and polymorphisms in fibroblast growth factor receptor 2
 RT (FGFR2) gene in humans.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE OF 314-427 FROM N.A.
 RX MEDLINE=20177482; PubMed=10712195;
 RA Glaser R.L., Jiang W., Boyadjev S.A., Tran A.K., Zachary A.A.,
 RA Van Maldergem L., Johnson D., Walsh S., Oldridge M., Wall S.A.,
 RA Wilkie A.O.M., Jabs E.W.;
 RT "Paternal origin of FGFR2 mutations in sporadic cases of Crouzon
 RT syndrome and Pfeiffer syndrome.";
 RL Am. J. Hum. Genet. 66:768-777(2000).
 RN [15]
 RP SEQUENCE OF 1-209; 212-767 AND 771-821 FROM N.A. (ISOFORMS 5; 14 AND
 RP 18).
 RX MEDLINE=99214070; PubMed=10196476;
 RA Zhang Y., Gorri M.C., Post J.C., Ehrlich G.D.;
 RT "Genomic organization of the human fibroblast growth factor receptor 2
 RT (FGFR2) gene and comparative analysis of the human FGFR gene family.";
 RL Gene 230:69-79(1999).
 RN [16]
 RP SEQUENCE OF 249-313 FROM N.A. AND VARIANTS AS TRP-252 AND ARG-253.
 RX MEDLINE=93397814; PubMed=7668257;
 RA Park W.-J., Theda C., Maestri N.E., Meyers G.A., Fryburg J.S.,
 RA Dufresne C., Cohen M.M. Jr., Jabs E.W.;
 RT "Analysis of phenotypic features and FGFR2 mutations in Apert
 RT syndrome.";
 RL Am. J. Hum. Genet. 57:321-328(1995).
 RN [17]
 RP SEQUENCE OF 251-259 FROM N.A.
 RX MEDLINE=96253074; PubMed=8676562;
 RA Wada C., Ishigaki M., Toyooka Y., Yamabe H., Ohnuki Y., Takada F.,
 RA Yamazaki Y., Ohtani H.;
 RT "Nucleotide sequences at intron 6 and exon 7 junction of fibroblast
 RT growth factor receptor 2 and rapid mutational analysis in Apert
 RT syndrome.";
 RL Rinsho Byori 44:435-438(1996).
 RN [18]
 RP SEQUENCE OF 251-318 FROM N.A.
 RX MEDLINE=96241572; PubMed=8673103;
 RA Moloney D.M., Slaney S.F., Oldridge M., Wall S.A., Sahlin P.,
 RA Stenman G., Wilkie A.O.M.;
 RT "Exclusive paternal origin of new mutations in Apert syndrome.";
 RL Nat. Genet. 13:48-53(1996).
 RN [19]
 RP SEQUENCE OF 263-361 FROM N.A. AND VARIANTS CS PRO-289; ARG-338;
 RP SER-342; TYR-342; GLY-344 AND CYS-354.
 RX MEDLINE=96090259; PubMed=7581378;
 RA Gorri M.C., Preston R.A., White G.J., Zhang Y., Singhal V.K.,
 RA Losken H.W., Parker M.G., Nwokoro N.A., Post J.C., Ehrlich G.D.;
 RT "Crouzon syndrome: mutations in two spliceforms of FGFR2 and a common
 RT point mutation shared with Jackson-Weiss syndrome.";
 RL Hum. Mol. Genet. 4:1387-1390(1995).
 RN [20]
 RP VARIANTS CS HIS-340; ARG-342; SER-342; TYR-342 AND CYS-354.
 RX MEDLINE=95078932; PubMed=7987400;
 RA Reardon W., Winter R.M., Rutland P., Pulleyn L.J., Jones B.M.,
 RA Malcolm S.;
 RT "Mutations in the fibroblast growth factor receptor 2 gene cause
 RT Crouzon syndrome.";
 RL Nat. Genet. 8:98-103(1994).

[21]
RN VARIANTS CS CYS-328 AND CYS-347, AND VARIANT JWS GLY-344.
RX MEDLINE=95179174; PubMed=7874170;
RA Jabs E.W., Li X., Scott A.F., Meyers G.A., Chen W., Eccles M., Mao J.,
RN Charnas L.R., Jackson C.E., Jaye M.;
RT "Jackson-Weiss and Crouzon syndromes are allelic with mutations in
RL fibroblast growth factor receptor 2.";
RN Nat. Genet. 8:275-279 (1994).
[22]
RN VARIANTS CS.
RX MEDLINE=95384152; PubMed=7655462;
RA Oldridge M., Wilkie A.O.M., Slaney S.F., Poole M.D., Pulleyn L.J.,
RN Rutland P., Hockley A.D., Wake M.J.C., Goldin J.H., Winter R.M.,
RA Reardon W., Malcolm S.;
RT "Mutations in the third immunoglobulin domain of the fibroblast growth
RL factor receptor-2 gene in Crouzon syndrome.";
RN Hum. Mol. Genet. 4:1077-1082 (1995).
[23]
RN VARIANTS CS GLY-290; TRP-342 AND CYS-354, AND VARIANT JWS ARG-342.
RX MEDLINE=96133301; PubMed=8528214;
RA Park W.-J., Meyers G.A., Li X., Theda C., Day D., Orlow S.J.,
RN Jones M.C., Jabs E.W.;
RT "Novel FGFR2 mutations in Crouzon and Jackson-Weiss syndromes show
Query Match 19.5%; Score 427; DB 1; Length 821;
Best Local Similarity 27.4%; Pred. No. 4.2e-25;
Matches 115; Conservative 84; Mismatches 167; Indels 54; Gaps 9;
QY 22 KQYEVIPTLL-----VTFLILLGVILMFIREQRTQOORSPQIGIA-----PV 67
Db 365 REKEBITASPDYLEIAIYICIGVFLIACMVVTIVILCRMKNNTKKPFSQPAVHKLTTRIPL 424
QY 68 PPRDLSSWAGHGNNALPLKETSVENFLGATTPALA-----KLVQVREQLSEV 116
Db 425 RRQTVSASSSSSNSNTPLVRIITRLSSDTATPMLAGVSEVELPEDPKWEPFRDKLT-L 483
QY 117 LEQICSGSCGPIFRANMNTGPSKPK---SVILKALKEPAGIHEVQDFLGRIOHQYILGK 173
Db 484 GKPLGEGCFQGVMAEAGVGDKEKPEAVTVAVKMKDDATEKDLVSEWEMKMKIGK 543
QY 174 HKNLVQEGCCTEKLPLMYLVEDVAQDGLLGLFWTCRRDVTMGLLYD-----LTE 225
Db 544 HKNINLLGACTQDGPYLVIVEYASKNRLREYLRARRPPGMEYS---YDINRVPEQMTF 600
QY 226 KQVYHIGKQVLLALEFLOEKHLFHGDVAARNLQSDLTAKLCGLGLA-----YEVY 277
Db 601 KDLVSCYVQARGMEYGLASQCIHRDLAARNVLTENNVMKIADPGLARDINNIDYKKT 660
QY 278 TRGAISSTQITPLKWLAPERLLLRPASIRADVMSFGILLYEMVTILGAPPYEVPPPTSILE 337
Db 661 TNG-----RLPVKMAPEALFDRVYTHQSDVMSFGVLMWEIFTLGSGSPYGPVPEELFK 714
QY 338 HLQRKIMKRSSCTHTMYSTKSCWRWREDRSPRELRLRLERAIAKTADDEAVLQVPE 397
Db 715 LLKRGHRMDKPNACTNLYMMRDCWHAVPSPQRTFKQVLEDLDRILTLTTNEEYLDLSQ 774

RESULT 9
FGRL_CHICK
ID FGRL_CHICK STANDARD; PRT; 819 AA.
AC P21804;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basic fibroblast growth factor receptor 1 precursor (BC 2.7.1.112).
GN CEK1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=893115814; PubMed=2473471;
RA Pasquale E.B., Singer S.J.;
RT "Identification of a developmentally regulated protein-tyrosine
RT kinase by using anti-phosphotyrosine antibodies to screen a CDNA
RT expression library.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5449-5453 (1989).
[2]
RN REVISIONS.
RA Pasquale E.B.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=89298406; PubMed=2544996;
RA Lee P.L., Johnson D.E., Cousens L.S., Fried V.A., Williams L.T.;
RT "Purification and complementary DNA cloning of a receptor for basic
RT fibroblast growth factor.";
RL Science 245:57-60 (1989).
CC -!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24637; AAA48663.1; --
CC FIR; A41345; TVCHFQ.
CC HSPF; P11362; IFGK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; Ig; 3.
DR PRINTS; PR00069; Dkinase; 1.
DR PROSITE; PS00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Transferrase; Phosphorylation; Transmembrane; Immunoglobulin domain;
KW Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 819
FT BASIC FIBROBLAST GROWTH FACTOR RECEPTOR
FT 1.
FT DOMAIN 22 374
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 375 395
FT POTENTIAL.
FT DOMAIN 396 819
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 118
FT IG-LIKE C2-TYPE 1.
FT DOMAIN 145 244
FT IG-LIKE C2-TYPE 2.
FT DOMAIN 253 355
FT IG-LIKE C2-TYPE 3.
FT DOMAIN 125 132
FT ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 476 765
FT PROTEIN KINASE.
FT NP_BIND 482 490
FT ACT SITE 512 512
FT BINDING 621 621
FT BY SIMILARITY.
FT MOD_RES 652 652
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT DISULFID 54 100
FT POTENTIAL.
FT DISULFID 176 228
FT POTENTIAL.
FT DISULFID 275 339
FT POTENTIAL.
FT CARBOHYD 76 76
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 90 90 A -> R (IN REF. 3).
 SQ SEQUENCE 819 AA; 91576 MW; 7E030B7AE5181DDC CRC64;

Query Match 19.3%; Score 424; DB 1; Length 819;
 Best Local Similarity 27.5%; Pred. No. 7.2e-25;
 Matches 112; Conservative 83; Mismatches 171; Indels 42; Gaps 8;

QY 25 EVIIVPTLLVTFLLIGLVILWLFTRQRTQOORSPQGIA-----PVPPPRDLSWEAG 78
 Db 374 EIIIVCT---GAFLISCWVTVIIYKMKSTTKTKDFNSQLAVHKAKSIPLRQVTVSAD 430

QY 79 HGNVALPIKETSVENFLGATTPALA-----KLQVREQ--LSEVLEQICSGSC 125
 Db 431 SSSNMNSGVMVLRPSRLSSGTPLAGVSEYELPEDPRWELPRDLRLGKPLGEGCFGQV 490

QY 126 GPIFRANWNTGDPKPKSVILKALKEPAGLHEVQDFLGRIOHQVQLGKHNVOLGCGCT 185
 Db 491 VLAEATGLDKKXPNRVTKAVKMLKSDATEKOLSLISEMMKMGKHKNIINLLGACT 550

QY 186 EXPLVMVLEDAVAGDLGLFWTCRDDVMTDGLLY-----DLTEKOVYHIGKV 235
 Db 551 QGPLYVIVYKSKNRLRYLQARR-----PPMEYCYNTPRIPEQSLFKDLVSCAYQV 605

QY 236 LLAELFLOEKHLFHGDVAARNILMOSDLPAKLCGLAVEVYTRGAISSTOT--IPLKWL 293
 Db 606 ARGMEYLASKKCIHRDLAARNVLVTEEDNMKADFGIARDIHHIDYKKTNGRLPVKWM 665

QY 294 APERILLRPASTRADVWSGILLYEMVTLGAPYVEPPTSLHLEHQRKIMKRPSSCTH 353
 Db 666 APEALFDRIYTHQSDVWSGILLYEFTLGGSPYFVGVPEELFKLKEGHRMDKPSNCTN 725

QY 354 TWYSIMKSCWRWRKRDPRRLRLRLLEAAIKTADDEAVLQVPELVVP 401
 Db 726 ELYMMRDCWHAVPQSRFTFKQVEDLDRIVAMTSNQEYL---DLVSP 770

RESULT 10

FGRL HUMAN
 ID FGRL HUMAN STANDARD; PRT; 822 AA.
 AC P11362; P17049; PRT; 822 AA.
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Basic fibroblast growth factor receptor 1 precursor (RC 2.7.1.112)
 DE (FGFR-1) (bFGF-R) (Fms-like tyrosine kinase-2) (c-fgr).
 GN FGFR1 OR FLG OR FGFR OR FLT2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90245600; PubMed=2159626;
 RA Isacchi A., Bergonzoni L., Sarnientos P.;
 RT "Complete sequence of a human receptor for acidic and basic
 RT fibroblast growth factors.";
 RL Nucleic Acids Res. 18:1906-1906(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neonatal brain stem;
 RX MEDLINE=90360977; PubMed=1697263;
 RA Dionne C.A., Crumley G.R., Bellot F., Kaplow J.M., Searfoss G.,
 RA Ruta M., Burgess W.H., Jaye M., Schlessinger J.;
 RT "Cloning and expression of two distinct high-affinity receptors,
 RT cross-reacting with acidic and basic fibroblast growth factors.";

RL EMBO J. 9:2685-2692(1990).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92282615; PubMed=1317750;
 RA Hattori Y., Odagiri H., Kato O., Sakamoto H., Morita T.,
 RA Shimotohno K., Tobinai K., Sugimura T., Terada M.;
 RT "K-sam-related gene, N-sam, encodes fibroblast growth factor receptor
 RT and is expressed in T-lymphocytic tumors.";
 RL Cancer Res. 52:3367-3371(1992).
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91126480; PubMed=1846977;
 RA Hou J., Kan M., McKeenhan K., McBride G., Adams P., McKeenhan W.L.;
 RT "Fibroblast growth factor receptors from liver vary in three
 RT structural domains.";
 RL Science 251:665-668(1991).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92118399; PubMed=1662973;
 RA Kiefer M.C., Baird A., George-Nascimento C., Nguyen T., Mason O.B.,
 RA Boley L.J., Valenzuela P., Barr P.J.;
 RT "Molecular cloning of a human basic fibroblast growth factor receptor
 RT cDNA and expression of a biologically active extracellular domain in
 RT a baculovirus system.";
 RL Growth Factors 5:115-127(1991).
 [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90290512; PubMed=2162671;
 RA Itoh N., Terachi T., Ohta M., Seo M.K.;
 RT "The complete amino acid sequence of the shorter form of human basic
 RT fibroblast growth factor receptor deduced from its cDNA.";
 RL Biochem. Biophys. Res. Commun. 169:680-685(1990).
 [7]
 RP SEQUENCE OF 201-822 FROM N.A.
 RA Ruta M., Howk R., Ricca G., Drohan W., Zabelshansky M., Laureys G.,
 RA Barton D.E., Francke U., Schlessinger J., Givol D.;
 RT "A novel protein tyrosine kinase gene whose expression is modulated
 RT during endothelial cell differentiation.";
 RL Oncogene 3:9-15(1988).
 [8]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=90355989; PubMed=2167437;
 RA Johnson D.E., Lee P.L., Lu J., Williams L.T.;
 RT "Diverse forms of a receptor for acidic and basic fibroblast growth
 RT factors.";
 RL Mol. Cell. Biol. 10:4728-4736(1990).
 [9]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=91141499; PubMed=1847500;
 RA Gutkind S.J., Link D.C., Katamine S., Lacal P., Miki T., Ley T.J.,
 RA Robbins K.C.;
 RT "A novel c-fgr exon utilized in Epstein-Barr virus-infected B
 RT lymphocytes but not in normal monocytes.";
 RL Mol. Cell. Biol. 11:1500-1507(1991).
 [10]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Lung;
 RX MEDLINE=91319400; PubMed=1650441;
 RA Eismann A., Ahn J.A., Graziani G., Tronick S.R., Ron D.;
 RT "Alternative splicing generates at least five different isoforms of
 RT the human basic-FGF receptor.";
 RL Oncogene 6:1195-1202(1991).
 [11]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [13]
RP MUTAGENESIS OF TYR-766.
RX MEDLINE=92357144; PubMed=1379697;
RA Peters K.G., Marie J., Wilson E., Ives H.E., Escobedo J.,
RA del Rosario M., Mirda D., Williams L.T.;
RT "Point mutation of an FGF receptor abolishes phosphatidylinositol
RT turnover and Ca²⁺ flux but not mitogenesis.";
RL Nature 358:678-681 (1992).
RN [14]
RP MUTAGENESIS OF TYR-766.
RX MEDLINE=92357145; PubMed=1379698;
RA Mohammad M., Dionne C.A., Li W., Lin N., Spivak T., Honegger A.M.,
RA Jaye M., Schlessinger J.;
RT "Point mutation in FGF receptor eliminates phosphatidylinositol
RT hydrolysis without affecting mitogenesis.";
RL Nature 358:681-684 (1992).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 464-762.
RX MEDLINE=96361355; PubMed=8752212;
RA Mohammad M., Schlessinger J., Hubbard S.R.;
RT "Structure of the FGF receptor tyrosine kinase domain reveals a novel
RT autoinhibitory mechanism.";
RL Cell 86:577-587 (1996).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 464-762.
RX MEDLINE=97284786; PubMed=9139660;
RA Mohammad M., McMahon G., Sun L., Tang C., Hirth P., Yeh B.K.,
RA Hubbard S.R., Schlessinger J.;
RT "Structures of the tyrosine kinase domain of fibroblast growth factor
RT receptor in complex with inhibitors.";
RL Science 276:955-960 (1997).
RN [17]
RP VARIANT PS ARG-252.
RX MEDLINE=95179173; PubMed=7874169;
RA Muenke M., Schell U., Hehr A., Robin N.H., Losken H.W., Schinzel A.,
RA Pulley L.J., Rutland P., Reardon W., Malcolm S., Winter R.M.;
RT "A common mutation in the fibroblast growth factor receptor 1 gene in
RT Pfeiffer syndrome.";
RL Nat. Genet. 8:269-274 (1994).
CC -!- FUNCTION: Receptor for basic fibroblast growth factor. A shorter
CC form of the receptor could be a receptor for acidic FGF (aFGF).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=7;
CC Comment-Additional isoforms seem to exist;
CC Name=Alpha A1;
CC IsoId=P11362-1; Sequence=Displayed;
CC Name=Alpha B1;
CC IsoId=P11362-2; Sequence=VSP_002960;
CC Name=Beta A1;
CC IsoId=P11362-3; Sequence=VSP_002958;
CC Name=Beta B1;
CC IsoId=P11362-4; Sequence=VSP_002958, VSP_002960;
CC Name=Gamma A1;
CC IsoId=P11362-5; Sequence=VSP_002957;
CC Name=Gamma B1;
CC IsoId=P11362-6; Sequence=VSP_002960;
CC Name=A;
CC IsoId=P11362-7; Sequence=VSP_002959;
CC -!- DISEASE: Defects in FGFR1 are one of the causes of Pfeiffer
CC syndrome (PS) [MIM:101600]; also known as acrocephalosyndactyly
CC type V (ACSV5). PS is characterized by craniosynostosis (premature
CC fusion of the skull sutures) with deviation and enlargement of the
CC thumbs and great toes, brachymesophalangy, with phalangeal
CC ankylosis and a varying degree of soft tissue syndactyly.
CC -!- DISEASE: Involved in a t(8;13)(p12;q12) chromosomal translocation
CC which involves FGFR1 and ZNF198. The resulting transcript is a
CC possible candidate for stem cell leukemia lymphoma syndrome/SCLL.
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/FGFR113.html".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

Query Match 19.3%; Score 424; DB 1; Length 822;
Best Local Similarity 30.2%; Pred. No. 7.2e-25;
Matches 97; Conservative 67; Mismatches 127; Indels 30; Gaps 5;
QY 100 TPALA-----KLQVREQ--LSEVLEQICSGSGPIFRANMTGDPSPKSVLL 146
DB 454 TPLAGVSEYELPDPRWELPRDLVLGKPGEGCGQVLAETGLDKDKPNRVTKAV 513
QY 147 KALKEPAGLHEVQDFLGFQHYLGKHNVLQLEGCCTEKPLVMVLEDAQGLLGL 206
DB 514 KMLKSDATEKLDLSISEMWMKMKGNINILGACTQDGLVIVYAYAGKGNREYL 573
QY 207 WTCRRDVMTMGLLY-----DLTEQVYHIGKQVLLALEFLQEKHLPHGDAARN 256
DB 574 QARR-----PPGLECYNPNHPQLSSKDLVSCAYQVARGMEYLASKKCIHRLAARN 628
QY 257 ILMQSDLTAKCGGLGAYEVYTRGALSSTQT--IPLKWLAPERILLRSPASVSGI 314
DB 629 VLVTEDNVMKADFGIARDIHHIDYKTKTNGRLPVMWAPALPDRIYTHQSDVMSFGV 688
QY 315 LLYEMVTLGAPPYEPVPTSLIEHLQRRKIMKRPSSCTHTMYSIMKSWRREADRPSR 374
DB 689 LLWEIFTLGSGPYGVPVEELFKLLKEGHRMDKPSNCTNELYMMWDCWHAVPSQRPTEK 748
QY 375 EURLLEAAIKTADAEAVLQV 395
DB 749 QLVEDLDRIVALTNSQEYLDL 769

RESULT 11
ABL_MLVAB
ID ABL_MLVAB STANDARD; PRT; 746 AA.
AC P00521;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase transforming protein ABL (BC 2.7.1.112).
GN V-ABL.
OS Abelson murine leukemia virus.
OX Viruses; Retroviridae; Mammalian type C retroviruses.
CX NCBI_TaxID=11788;
RN [1]_TaxID=11788;
RP SEQUENCE FROM N.A.
RX MEDLINE=83221648; PubMed=6304726;
RA Reddy E.P., Smith M.J., Srinivasan A.;
RT "Nucleotide sequence of Abelson murine leukemia virus genome."

RT structural similarity of its transforming gene product to other onc
RT gene products with tyrosine-specific kinase activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3623-3627(1983).
RN [2]
RN REVISIONS TO 588-746.
RA Reddy E.P., Smith M.J., Srinivasan A.;
RL Proc. Natl. Acad. Sci. U.S.A. 80:7372-7372(1983).
RN [3]
RP SEQUENCE OF 233-327 FROM N.A.
RX MEDLINE=83245023; PubMed=6191223;
RA Groffen J., Heisterkamp N., Reynolds F.H. Jr., Stephenson J.R.;
RT "Homology between phosphotyrosine acceptor site of human c-abl and
RT viral oncogene products";
RL Nature 304:167-169(1983).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ABL
CC POLYPEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; V01541; -; NOT ANNOTATED_CDS.
DR EMBL; K00010; AAA46470.1; -;
DR HSSP; P00519; 2ABL;
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_pkinase_A5.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PD000001; Prot_kinase; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
KW Polyprotein; Transferase; Tyrosine-protein kinase; ATP-binding;
KW Oncogene; SH2 domain.
FT DOMAIN 13 103 SH2
FT DOMAIN 128 379 PROTEIN_KINASE.
FT NP_BIND 134 142 ATP (BY SIMILARITY).
FT BINDING 157 157 ATP (BY SIMILARITY).
FT ACT_SITE 249 249 BY SIMILARITY.
SQ SEQUENCE 746 AA; 81872 MW; B9072FFP55PE9257 CRC64;

Query Match 19.1%; Score 419; DB 1; Length 746;
Best Local Similarity 34.7%; Pred. No. 1.5e-24;
Matches 96; Conservative 51; Mismatches 94; Indels 36; Gaps 7;

QY 143 SVILKALKEPAGLHEVDLGRIFQFHYGLKHKHNLVQLGECCKEPLPLYWVLEDAVQGLD 202
DB 153 TVAVKTLKEDT--MEVEEFLKEAAVKKEL-KHENLVQLLGVCVTRPFPFFIITEFTYGNL 209
QY 203 LGFLWTCRRDVMTMDGLDYLTEKQVYVHGKQVLLALEFLQEKHLPFGVDAARNILMQSD 262
DB 210 LDVIRECNRQEVSAVLLYMAT-----QISSAMEYLEKKNFTHRLAARNCLVGEN 260
QY 263 LFAKLCGLGLAY-----EVVTRGAISSQTQITPLKWLAPERLLLRPASIRADVWSFGILLYE 318
DB 261 HLVKVADFGLRLMTGDTYTAHAGAK---FPFKWTAPESLAYNKFISKSDVWAFGLLWE 317

QY 319 MYTLGAPPYEPVPTSIILEHLORRKIMKRPSCCTHTMYSIMKSWREARSPRELRL 378
DB 318 IATYGMSPYGDLSQVIELLEKDYRMERPECKPEKYMELMRACWQNFSDRPSFAEIHQ 377
QY 379 RLEAAIK--TADDE-----AVLQVPEL 398
DB 378 AFETMFQESSISDEVEKEIGKRGTRGGAGSMLOAPEL 414

RESULT 12
ABL1 MOUSE
ID ABL1 MOUSE STANDARD; PRT; 1123 AA.
AC P00520; P97896; Q61252; Q61253; Q61254; Q61255; Q61256; Q61257;
AC Q61258; Q61259; Q61260; Q61261;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase ABL1 (EC 2.7.1.112) (p150)
DE (c-ABL).
GN ABL1 OR ABL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomii;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=88068561; PubMed=3317402;
RA Oppi C., Shore S.K., Reddy E.P.;
RT "Nucleotide sequence of testis-derived c-abl cDNAs: implications for
RT testis-specific transcription and abl oncogene activation";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8200-8204(1987).
RN [2]
RP SEQUENCE OF 1-187 FROM N.A. (ISOFORMS I; II; III AND IV).
RX MEDLINE=95394474; PubMed=7665185;
RA Chisoe S.L., Bodenteich A., Wang Y.-F., Wang Y.-P., Burian D.,
RA Clifton S.W., Crabtree J., Freeman A., Iyer K., Jian L., Ma Y.,
RA McLaury H.-J., Pan H.-Q., Sarhan O.H., Toth S., Wang Z., Zhang G.,
RA Heisterkamp N., Groffen J., Roe B.A.;
RT "Sequence and analysis of the human ABL gene, the BCR gene, and
RT regions involved in the Philadelphia chromosomal translocation";
RL Genomics 27:67-82(1995).
RN [3]
RP SEQUENCE OF 85-182 FROM N.A.
RX MEDLINE=84106840; PubMed=6319018;
RA Wang J.Y.J., ledley F., Goff S., Lee R., Groner Y., Baltimore D.;
RT "The mouse c-abl locus: molecular cloning and characterization";
RL Cell 36:349-356(1984).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=88202920; PubMed=3283651;
RA Bernards A., Paskind M., Baltimore D.;
RT "Four murine c-abl mRNAs arise by usage of two transcriptional
RT promoters and alternative splicing";
RL Oncogene 2:297-304(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 61-121.
RX MEDLINE=95393198; PubMed=7664083;
RA Musacchio A., Saraste M., Wilmanns M.;
RT "High-resolution crystal structures of tyrosine kinase SH3 domains
RT complexed with proline-rich peptides";
RL Nat. Struct. Biol. 1:546-551(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 229-515.
RX MEDLINE=2046271; PubMed=1098075;
RA Schindler T., Bornmann W., Pellicena P., Miller W.T., Clarkson B.,
RA Kuriyan J.;
RT "Structural mechanism for Src-571 inhibition of abelson tyrosine
RT kinase";
RL Science 289:1938-1942(2000).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.

GO; GO:0008630; P:DNA damage response, signal transduction re. . .; TAS.
 GO; GO:0006298; P:mismatch repair; TAS.
 GO; GO:0000074; P:regulation of cell cycle; TAS.
 GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
 GO; GO:0000115; P:S-specific transcription in mitotic cell cycle; TAS.
 InterPro; IPR000719; Prot_kinase.
 InterPro; IPR000980; SH2.
 InterPro; IPR001452; SH3.
 InterPro; IPR001245; Tyr_pkinase.
 InterPro; IPR008266; Tyr_pkinase_AS.
 Pfam; PF00069; pkinase; 1.
 Pfam; PF00017; SH2; 1.
 Pfam; PF00018; SH3; 1.
 PRINTS; PR00401; SH2DOMAIN.
 PRINTS; PR00452; SH3DOMAIN.
 PRINTS; PR00109; TYRKINASE.
 ProDom; PD000001; Prot_kinase; 1.
 ProDom; PD000093; SH2; 1.
 ProDom; PD000066; SH3; 1.
 SMART; SM00252; SH2; 1.
 SMART; SM00326; SH3; 1.
 SMART; SM00219; TyrKc; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 PROSITE; PS00001; SH2; 1.
 PROSITE; PS00002; SH3; 1.
 Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 Phosphorylation; SH2 domain; SH3 domain; Chromosomal translocation;
 3D-structure; Alternative splicing.
 DOMAIN 61 121
 DOMAIN 127 217
 DOMAIN 242 493
 DOMAIN 605 609
 DOMAIN 18 22
 DOMAIN 605 609
 DOMAIN 782 1019
 DOMAIN 897 903
 SITE 26 27
 NP_BIND 248 256
 BINDING 271 271
 ACT_SITE 363 363
 MOD_RES 393 393
 VARSPPLIC 1 26
 Query Match 19.0%; Score 417; DB 1; Length 1130;
 Best Local Similarity 34.7%; Pred. No. 3.8e-24;
 Matches 96; Conservative 49; Mismatches 96; Indels 36; Gaps 7;
 QY 143 SVILKALKEPAGLHVEDPFLGRIQPHOYLGHKHLVLEGCTCKPLVMVLEDAVQGD 202
 Db 267 TVAVTKLEDT--MEVEFLKEAAMVKET-RHPLNVQLGVCTREPPPIITFTFYGNL 323
 QY 203 LGFLWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALEFLQEHKLFHGDVAARNILMQSD 262
 Db 324 LDYLRECNQEVNAVLLYMAI-----QISSAMEYLEKKNFIHDLAARNCLVGEN 374
 QY 263 LTAKLCGLGLAY----EYVTGATISSTQIPKWLAPERLLLRPASTRADVWVSGILLYE 318
 Db 375 HLNVKVDAPGLSRLMTGDTYTAHAKA---FFIKWTAPESLAYNKFISKSDVWAFGLVWE 431
 QY 319 MVTGLGAPPYVPPTSLIEHLQRRKIMKRBPSSCTHTWYSIMKSCWRWEADRPSPRELRL 378
 Db 432 IATYQMSYPGIDUSQVYELLEKVDYMERPECPKVVYELMRACQWNPSPRPSAEIHQ 491
 QY 379 RLEAAIK--TADDE-----AVLQVPEL 398
 Db 492 AFEITMFOESSISDEVEKELGKQVGVASTLLQAPEL 528
 RESULT 14

FGRL1 XENLA STANDARD; PRT; 812 AA.
 AC P22182;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibroblast growth factor receptor 1 precursor (EC 2.7.1.112).
 GN FGFR-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91045998; PubMed=2172985;
 RA Musci T.J., Amaya E., Kirschner M.W.;
 RT "Regulation of the fibroblast growth factor receptor in early Xenopus
 embryos.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8365-8369(1990).
 CC -!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
 CC family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; U24491; AAA86968.1; .
 DR PIR; A36477; A36477.
 DR HSP; P11362; IFCK.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
 KW Transferrase; Phosphorylation; Transmembrane; Immunoglobulin domain;
 KW Repeat; Signal.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 812 FIBROBLAST GROWTH FACTOR RECEPTOR 1.
 FT DOMAIN 21 371 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 372 393 POTENTIAL.
 FT DOMAIN 394 812 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 33 110 IG-LIKE C2-TYPE 1.
 FT DOMAIN 154 242 IG-LIKE C2-TYPE 2.
 FT DOMAIN 251 353 IG-LIKE C2-TYPE 3.
 FT DOMAIN 472 761 PROTEIN KINASE.
 FT NP_BIND 478 486 ATP (BY SIMILARITY).
 FT BINDING 508 508 ATP (BY SIMILARITY).
 FT ACT_SITE 617 617 BY SIMILARITY.
 FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).

```

CC CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 812 AA; 90502 MW; B06333BAFACSC9B CRC64;

Query Match 19.0%; Score 416; DB 1; Length 812;
Best Local Similarity 29.7%; Pred. No. 2.9e-24;
Matches 97; Conservative 67; Mismatches 137; Indels 26; Gaps 5;

QY 92 VENFLGATTPALAKU-----QVPEQ--LSEVLEQICSGCGPIFRANMTGDP 138
DB 440 VRLSSSGTFLMSGLSEYELPDPNWEVARDRLILCKPLGEGCGVQVMAEALGDKERP 499

QY 139 SKPKSVILKALKEPAGLHEVQDFLGRIOFHYGLGKHNLVLEGCGCTEKLPLYMVEDVA 198
DB 500 NKVTKVAVKMLKSDASEKDLSDISEMMMKMGKHNIINLLGACTQDGLYVIVEYTS 559

QY 199 QGDLGLFWT-----CRDVMTMDGLLYDLTEKQVYHIGKQVLLALEEQLKHLPHG 250
DB 560 KGNLEYLRRARPPAMEYCYNTCPDQL---LSFKDLVSCAYQVARGMDYLASKKCIHR 616

QY 251 DVAARNILMQSDILAKLGLGLGAYEVYTRGAISSTQT--IPLKWLAPERLLLRPASIRAD 308
DB 617 DIAARNVLTEDNIMKIADFGIARDIHHIDYKKTNGRLPVKMAPEALFDRIYTHQSD 676

QY 309 VMSFGILLVEMTVLGAPPVPEPPTSILEHLQRRKMKRPSCTHTMYIMSKSWRRA 368
DB 677 VMSFGILLWEITFGSPGPGVMEBLFKLKEGHRMDKPTNCTNELYMMKDCWHAMPS 736

QY 369 DRPSPELRLEAAIKTADDEAVLQV 395
DB 737 QRPTFNQVLVEDLRILALSSNQEYDDL 763

RESULT 15
FGP1_RAT
ID FGP1_RAT STANDARD; PRT; 822 AA.
AC Q04589;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basic fibroblast growth factor precursor 1 precursor (EC 2.7.1.112)
DE (FGFR-1) (bFGF-R) (MFR).
GN FGFR1 OR FLG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=93176824; PubMed=8382532;
RA Yazaki N., Hiroko F., Mitsuhiro O., Toshihiko K., Nobuyuki I.;
RT "The structure and expression of the FGF receptor-1 mRNA isoforms in
RT rat tissues.";
RL Biochim Biophys. Acta 1172:37-42(1993).
CC -!- FUNCTION: Receptor for basic fibroblast growth factor. A shorter
CC form of the receptor could be a receptor for acidic FGF (aFGF).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
```

```

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; D12498; BAA02059.1; -
CC HSP; S29840; S29840.
CC PIR; P11362; IFGK.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003598; Ig_c2.
CC DR InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR001245; Tyr_kinase.
CC DR Pfam; PF00047; Ig; 3.
CC DR Pfam; PF00069; pkinase; 1.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR SMART; SM00408; Igc2; 3.
CC DR SMART; SM00219; TyrKc; 1.
CC DR PROSITE; PS00835; IG_LIKE; 3.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
CC KW Transferase; Phosphorylation; Transmembrane; Signal;
CC KW Immunoglobulin domain; Repeat.
CC FT SIGNAL 1 21
CC FT CHAIN 22 822
CC FT DOMAIN 22 376
CC FT TRANSMEM 377 376
CC FT DOMAIN 398 822
CC FT DOMAIN 25 119
CC FT DOMAIN 158 246
CC FT DOMAIN 255 357
CC FT DOMAIN 478 767
CC FT NP_BIND 484 492
CC FT BINDING 514 514
CC FT ACT_SITE 623 623
CC FT MOD_RES 654 654
CC FT DISULFID 55 101
CC FT DISULFID 178 230
CC FT DISULFID 277 341
CC FT CARBOHYD 77 77
CC FT CARBOHYD 117 117
CC FT CARBOHYD 227 227
CC FT CARBOHYD 240 240
CC FT CARBOHYD 264 264
CC FT CARBOHYD 296 296
CC FT CARBOHYD 317 317
CC FT CARBOHYD 330 330
CC SQ SEQUENCE 822 AA; 91824 MW; E59D92AD0AIDE5C5 CRC64;

Query Match 18.9%; Score 415; DB 1; Length 822;
Best Local Similarity 29.9%; Pred. No. 3.6e-24;
Matches 96; Conservative 67; Mismatches 128; Indels 30; Gaps 5;

QY 100 TPALA-----KLQVPEQ--LSEVLEQICSGCGPIFRANMTGDPSPKSVIL 146
DB 454 TEMPLAGVSEYELPDPNWEVARDRLILCKPLGEGCGVQVMAEALGDKKPNRTKVAV 513

QY 147 KALKEPAGLHEVQDFLGRIOFHYGLGKHNLVLEGCGCTEKLPLYMVEDVAQDGLLGL 206
DB 514 KMLKSDATEKDLSDISEMMMKMGKHNIINLLGACTQDGLYVIVEYTSKGNLREYL 573

QY 207 WTCCRDRVMTMDGLLY-----DLTEKQVYHIGKQVLLALEEQLKHLFHDVVAARN 256
DB 574 QARR-----PPGLEVCYNPSHNPEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARN 628

QY 257 ILMQSDILAKLGLGAYEVYTRGAISSTQT--IPLKWLAPERLLLRPASIRADVWSFGI 314
DB 629 VLVETEDNMKIADFGIARDIHHIDYKKTNGRLPVKMAPEALFDRIYTHQSDVWSFGV 698

QY 315 LLVEMTVLGAPPVPEPPTSILEHLQRRKMKRPSCTHTMYIMSKSWRREADRPSPR 374
```

Db 689 LLWEFTLGGSPNPGVPVEELFKLLKEGHRMDKPSNCTNELYMMWRDCWNAVPSQRPTEK 748

QY 375 ELRLRLAAIKTADDEAVLQV 395

Db 749 QLVEDLDRIVALTSNQEYLDL 769

Search completed: June 14, 2004, 18:44:46
Job time : 19 secs

This Page Blank (usp:0)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 18:42:14 ; Search time 20 Seconds
(without alignments)
2029.641 Million cell updates/sec

Title: US-10-040-884-3
Perfect score: 2192
Sequence: 1 MGMTMLLECSLSDKLCVIQ.....LYAAVAGIRVESLFYNSML 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2192	100.0	422	T48680	hypothetical prote
2	465.5	21.2	829	JC4583	fibroblast growth
3	459.5	21.0	818	JC4058	fibroblast growth
4	455.5	20.8	822	S19947	fibroblast growth
5	455.5	20.8	822	B49151	fibroblast growth
6	453.5	20.7	800	TVHU2F	fibroblast growth
7	453.5	20.7	800	A48991	heparin-binding gr
8	447	20.4	797	S38579	fibroblast growth
9	446.5	20.4	806	A35963	protein-tyrosine k
10	444	20.3	801	I53363	fibroblast growth
11	444	20.3	806	TVHUF3	fibroblast growth
12	439.5	20.1	713	I50128	fibroblast growth
13	434	19.8	802	TVHUF4	fibroblast growth
14	433	19.8	705	S51635	fibroblast growth
15	433	19.8	707	A38429	keratinocyte growt
16	433	19.8	820	S17295	fibroblast growth
17	433	19.8	821	TVMSBK	fibroblast growth
18	432	19.7	682	A35969	heparin-binding gr
19	432	19.7	733	I43293	fibroblast growth
20	432	19.7	822	I42889	fibroblast growth
21	431	19.7	799	S18209	fibroblast growth
22	430	19.6	707	A54846	fibroblast growth
23	430	19.6	729	A56795	fibroblast growth
24	430	19.6	822	B54846	fibroblast growth
25	427.5	19.5	822	1 TVMSFG	fibroblast growth
26	427	19.5	821	1 TVHUF2	fibroblast growth
27	427	19.5	822	2 A45081	fibroblast growth
28	426	19.4	822	2 A41794	keratinocyte growt
29	424.5	19.4	832	2 JH0393	fibroblast growth

30	424	19.3	819	1 TVCHFG	fibroblast growth
31	424	19.3	822	1 TVHUEG	fibroblast growth
32	423	19.3	769	2 S16236	fibroblast growth
33	423	19.3	814	1 A39752	fibroblast growth
34	421	19.2	650	1 JC1450	fibroblast growth
35	419	19.1	981	1 FOMVGM	gag-abl polyprotei
36	419	19.1	1123	2 A39962	kinase-related tra
37	418	19.1	824	2 S36439	fibroblast growth
38	417	19.0	415	2 I65223	heparin-binding fi
39	417	19.0	1130	1 TVHUA	protein-tyrosine k
40	416	19.0	812	1 A36477	fibroblast growth
41	415	18.9	748	2 S41050	fibroblast growth
42	415	18.9	750	2 S41051	fibroblast growth
43	415	18.9	822	2 S29840	fibroblast growth
44	415	18.9	823	2 B35963	protein-tyrosine k
45	412	18.8	824	2 S24108	protein-tyrosine k

ALIGNMENTS

RESULT 1

T48680
hypothetical protein DKFZp761P1010.1 - human
C:Species: Homo sapiens (man)
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C:Accession: T48680
R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24533
A:Accession: T48680
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-422 <AAA>
A:Cross-references: EMBL:AL353940
A:Experimental source: adult amygdala; clone DKFZp761P1010
C:Genetics:
A>Note: DKFZp761P1010.1

Query Match		100.0%;	Score 2192;	DB 2;	Length 422;
Best Local Similarity		100.0%;	Pred. No. 6.2e-103;		
Matches 422;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGMTMLLECSLSDKLCVIQEQYEVIVPTLLVTIFILLGLVILWLFIREORTQQQSG	60		
Db	1	MGMTMLLECSLSDKLCVIQEQYEVIVPTLLVTIFILLGLVILWLFIREORTQQQSG	60		
Qy	61	PQGIAPVPPRDLSSWEAGHGGNVALPLKETSVENFGLGATTPALAKLQVPREQLSEVLBQI	120		
Db	61	PQGIAPVPPRDLSSWEAGHGGNVALPLKETSVENFGLGATTPALAKLQVPREQLSEVLBQI	120		
Qy	121	CSGSGCPIFRANMTGDPSPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGHKNLVQL	180		
Db	121	CSGSGCPIFRANMTGDPSPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGHKNLVQL	180		
Qy	181	EGCCTEKLPLWVLEDAQGLLGLFWTCRDDVMTDGLLYDLTEKQVYHIGKVLLALE	240		
Db	181	EGCCTEKLPLWVLEDAQGLLGLFWTCRDDVMTDGLLYDLTEKQVYHIGKVLLALE	240		
Qy	241	FLQEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQTTPLKWLAPERLLL	300		
Db	241	FLQEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQTTPLKWLAPERLLL	300		
Qy	301	RPASTRADVWFGILLYEMVTILGAPPYEPVPTSLIEHLQRRKIMKRPSCHTHMYSIMK	360		
Db	301	RPASTRADVWFGILLYEMVTILGAPPYEPVPTSLIEHLQRRKIMKRPSCHTHMYSIMK	360		
Qy	361	SCWRREADRSPRELRLLEAAIKTADDEAVLQVPELVVPELVAAVAGIRVESLFYNS	420		
Db	361	SCWRREADRSPRELRLLEAAIKTADDEAVLQVPELVVPELVAAVAGIRVESLFYNS	420		
Qy	421	ML 422			

Db 421 ML 422

RESULT 2

JC4583
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 16-Jul-1999
 C:Accession: JC4583
 R.Riou, J.F.; Clavilier, L.; Boucaut, J.C.
 Biochem. Biophys. Res. Commun. 218, 198-204, 1996
 A>Title: Early regionalized expression of a novel Xenopus fibroblast growth factor receptor
 A:Reference number: JC4583; MUID:96136300; PMID:8573131
 A:Accession: JC4583
 A:Molecule type: mRNA
 A:Residues: 1-829 <RIO>
 A:Cross-references: EMBL:X89807
 A:Experimental source: embryo
 C:Comment: This receptor is a tyrosine kinase transmembrane protein and plays an important role in the development of the embryo.
 C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase
 C:Keywords: ATP; embryo; fibroblast; growth factor; receptor; transmembrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-829/Product: fibroblast growth factor receptor 4B #status predicted <MAT>
 F:60-117/Domain: immunoglobulin homology <IM1>
 F:136-148/Region: acidic
 F:187-251/Domain: immunoglobulin homology <IM2>
 F:287-362/Domain: immunoglobulin homology <IM3>
 F:393-413/Domain: transmembrane #status predicted <TM>
 F:488-773/Domain: protein kinase homology <KIN>
 F:496-504/Region: protein kinase ATP-binding motif

Query Match 21.2%; Score 465.5; DB 2; Length 829;
 Best Local Similarity 29.4%; Pred. No. 2e-16;
 Matches 118; Conservative 82; Mismatches 171; Indels 31; Gaps 11;

```

QY 21 EKQYEVIIVPT--LLVTIFLLILGLVILWFIREQRTQQRSGPQGIAPVPPPRDLSWEAG 78
Db 387 ESKYMDIIITYTSGFLAVAMAIVILCRMQTPHKSQTLPPTVHKLAKFPLIRQFSLESS 446

QY 79 HGGNVALPL-KETSVENFLGATTPAL-----AKLQVPRQLSEVL-EQICSSGCGPI 128
Db 447 SSGKSSAPLIRITRLSSSCAPMLPGVMEVELPLDAKWEPPDRLL--VLGKPLGEGCFGQV 504

QY 129 FRA---NMNTGDPSPKPKSVILKALKEPAGLHVQDFLGRIOHQHYLGKHKNLVOLGECCT 185
Db 505 VRAEGVGIKDEPKPEKPTVAVVVKLKDNGTDKLSLISEMLMKVIGKHKNIINLGVST 564

QY 186 EKLLPMVLEDAVQDGLLGLFWTCRRDVMTDGLLYDLTE-----KQVYHIGKQVLL 237
Db 565 QEGPLFVIVEYASKGNLREFL--RARRPTPEDA--FDITKVPDELLSPKDLVSCAYQVAR 621

QY 238 ALFETQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEVYTRGASISSTQT--IPLKWLAP 295
Db 622 GMEYLESKRCIHRDLAARNLVVAEDNVKMIADFGIARGVHDIDYKYKTSNGRLPKVKNWAP 681

QY 296 ERLILRPASIRADVMSFGILLVEMVTLGAPPYVPEPPTSILEHLQRRKIMKPPSSCTHTM 355
Db 682 EALFDRVYTHQSDIWSFGVLTWEITLGGSPYPIYPELFLKLLRGHRMDKPSNCTHEL 741

QY 356 YSIMKSCWRWRADRPSPRELRLRLAEAAIKTADDEAV-IQVP 396
Db 742 YMLMECHHVAVPTQPTFKQLVEQLDRILITAVSSEYDLDSMP 783

```

RESULT 3

JC4058
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000
 C:Accession: JC4058
 R.Shiozaki, C.; Tashiro, K.; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiohawa, K.
 Gene 152, 215-219, 1995
 A>Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor-4

A:Reference number: JC4058; MUID:95137391; PMID:7835703

A:Accession: JC4058

A:Molecule type: mRNA

A:Residues: 1-818 <SHI>

A:Cross-references: DDBJ:D31761; NID:g809527; PIDN:BAA06539.1; PID:g809528

C:Genetics:

A:Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 429/1; 478/1; 556/1; 619/1; 680/1
 C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase
 C:Keywords: ATP; growth factor receptor; transmembrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-818/Product: fibroblast growth factor receptor-4 #status predicted <MAT>

F:56-110/Domain: immunoglobulin homology <IM1>
 F:132-137/Domain: acidic #status predicted <ADI>
 F:177-238/Domain: immunoglobulin homology <IM2>
 F:276-347/Domain: immunoglobulin homology <IM3>
 F:382-402/Domain: transmembrane #status predicted <TM>
 F:477-762/Domain: protein kinase homology <KIN>
 F:485-493/Region: protein kinase ATP-binding motif

Query Match 21.0%; Score 459.5; DB 2; Length 818;

Best Local Similarity 29.4%; Pred. No. 4e-16;

Matches 118; Conservative 83; Mismatches 170; Indels 31; Gaps 11;

```

QY 21 EKQYEVIIVPT--LLVTIFLLILGLVILWFIREQRTQQRSGPQGIAPVPPPRDLSWEAG 78
Db 376 ESKYMDIIITYTSGFLAVAMAIVIVLCRMQTPHKSQTLPQPPAVHKLAKFPLIRQFSLESS 435

QY 79 HGGNVALPL-KETSVENFLGATTPAL-----AKLQVPRQLSEVL-EQICSSGCGPI 128
Db 436 SSGKSSAPLIRITRLSSSCAPMLPGVMEVELPLDAKWEPPDRLL--VLGKPLGEGCFGQV 493

QY 129 FRA---NMNTGDPSPKPKSVILKALKEPAGLHVQDFLGRIOHQHYLGKHKNLVOLGECCT 185
Db 494 VRAEGVGIKDEPKPEKPTVAVVVKLKDNGTDKLSLISEMLMKVIGKHKNIINLGVST 553

QY 186 EKLLPMVLEDAVQDGLLGLFWTCRRDVMTDGLLYDLTE-----KQVYHIGKQVLL 237
Db 554 QEGPLFVIVEYASKGNLREFL--RARRPTPEDA--FDITKVPDELLSPKDLVSCAYQVAR 610

QY 238 ALFETQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEVYTRGASISSTQT--IPLKWLAP 295
Db 611 GMEYLESKRCIHRDLAARNLVVAEDNVKMIADFGIARGVHDIDYKYKTSNGRLPKVKNWAP 670

QY 296 ERLILRPASIRADVMSFGILLVEMVTLGAPPYVPEPPTSILEHLQRRKIMKPPSSCTHTM 355
Db 671 EALFDRVYTHQSDIWSFGVLTWEITLGGSPYPIYPELFLKLLRGHRMDKPSNCTHEL 730

QY 356 YSIMKSCWRWRADRPSPRELRLRLAEAAIKTADDEAV-IQVP 396
Db 731 YMLMECHHVAVPSQPTFKQLVEQLDRILITAVSSEYDLDSMP 772

```

RESULT 4

S19947
 C:Species: Pleurodeles waltlii (Iberian ribbed newt)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S19947
 R.Shii, D.L.; Feige, J.J.; Riou, J.F.; DeSimone, D.W.; Boucaut, J.C.
 submitted to the EMBL Data Library, March 1992
 A:Description: Receptors during early development of the urodele Pleurodeles waltlii.
 A:Reference number: S19947
 A:Accession: S19947
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-822 <SHI>
 A:Cross-references: EMBL:X65059
 C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase
 C:Keywords: ATP; growth factor receptor
 F:283-354/Domain: immunoglobulin homology <IM>
 F:484-769/Domain: protein kinase homology <KIN>
 F:492-500/Region: protein kinase ATP-binding motif

```
Query Match      20.8%; Score 455.5; DB 2; Length 822;
Best Local Similarity 29.2%; Pred. No. 6.3e-16;
Matches 118; Conservative 82; Mismatches 169; Indels 35; Gaps 11;

QY 21 EKQYEVIIVPT--LLVTFILLLGVILWLFIREORTQOORSGPQGIAPVPPPRDLWSWAG 78
DB 383 ETRYTDIIITYTSGSLALLMAAVIVVLCRMQLPPTKTHLEPATVHKLSRFPLMRQPSLESS 442
QY 79 HGGNVALPLKETSVENFGLATTPAL-----AKLQVPREOLSEVL--EQICSGSGC 126
DB 443 SSGKSTSL--VRVTRLSSCTPMLPGVLEFDLPDLSKWEFFPREL--VLGKPLGEGCFG 498
QY 127 PIFRA---NMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOFQHYLGKHNVLQLEG 183
DB 499 QVRAEAGINKDQDKAITVAIKIVKDKGTDELSDLISEMELMKMGKHNIIINLLGV 558
QY 184 CTEKPLPLMWLEDAVQAQDGLLGLFWTCRRDVTMTDGLLYDLTE-----KQVYHIGKQV 235
DB 559 CTQDGPLYMIWEYASKGNLREFL--RARRP--PSPDYTFDMTKVPEQLSFQDLVSCSYQV 615
QY 236 LLALEFLOEKHLFGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWL 293
DB 616 ARGWAYLESKRCIHRDLAARNVLTGENVMKIADPGLARGVHDIDYKKTSNGRLPVKWM 675
QY 294 APERILLRPAIRADVMSFGILLYEMVTILGAPPYVEVPPTSIHLQRRKMKRPSSCTH 353
DB 676 APEALFDRVYTHQSDVMSFGVLTWEIFTLGSGPYGIPVEELFKLLRGHRMDKPSNCTH 735
QY 354 TMSIMKSCWWRADRPSPRELRLRLLEAAIKTADDEAV--LQVP 396
DB 736 ELYMLMRECWAHAPSQRPTFKQLVETLDRILATVAEEYLDLSMP 779

RESULT 5
B49151
fibroblast growth factor receptor 4 - Iberian ribbed newt
C:Species: Pleurodeles waltlii (Iberian ribbed newt)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: B49151
R:Shi, D.L.; Feige, J.J.; Riou, J.F.; DeSimone, D.W.; BoucAUT, J.C.
Development 116, 261-273, 1992
A:Title: Differential expression and regulation of two distinct fibroblast growth factor
A:Reference number: A49151; MUID:93130775; PMID:1483392
A:Accession: B49151
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-822 <SHI>
A:Cross-references: GB:X65059; NID:G64252; PIDN:CAA46192.1; PID:G64253
A:Experimental source: tail-bud
A:Note: sequence extracted from NCBI backbone (NCBIN:122598, NCBIp:122599)
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C:Keywords: ATP; growth factor receptor
F:283-354/Domain: immunoglobulin homology <IMM>
F:484-769/Domain: protein kinase homology <KIN>
F:492-500/Region: protein kinase ATP-binding motif

Query Match      20.8%; Score 455.5; DB 2; Length 822;
Best Local Similarity 29.2%; Pred. No. 6.3e-16;
Matches 118; Conservative 82; Mismatches 169; Indels 35; Gaps 11;

QY 21 EKQYEVIIVPT--LLVTFILLLGVILWLFIREORTQOORSGPQGIAPVPPPRDLWSWAG 78
DB 383 ETRYTDIIITYTSGSLALLMAAVIVVLCRMQLPPTKTHLEPATVHKLSRFPLMRQPSLESS 442
QY 79 HGGNVALPLKETSVENFGLATTPAL-----AKLQVPREOLSEVL--EQICSGSGC 126
DB 443 SSGKSTSL--VRVTRLSSCTPMLPGVLEFDLPDLSKWEFFPREL--VLGKPLGEGCFG 498
QY 127 PIFRA---NMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOFQHYLGKHNVLQLEG 183
DB 499 QVRAEAGINKDQDKAITVAIKIVKDKGTDELSDLISEMELMKMGKHNIIINLLGV 558
QY 184 CTEKPLPLMWLEDAVQAQDGLLGLFWTCRRDVTMTDGLLYDLTE-----KQVYHIGKQV 235
```

```
DB 559 CTQDGPLYMIWEYASKGNLREFL--RARRP--PSPDYTFDMTKVPEQLSFQDLVSCSYQV 615
QY 236 LLALEFLOEKHLFGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWL 293
DB 616 ARGWAYLESKRCIHRDLAARNVLTGENVMKIADPGLARGVHDIDYKKTSNGRLPVKWM 675
QY 294 APERILLRPAIRADVMSFGILLYEMVTILGAPPYVEVPPTSIHLQRRKMKRPSSCTH 353
DB 676 APEALFDRVYTHQSDVMSFGVLTWEIFTLGSGPYGIPVEELFKLLRGHRMDKPSNCTH 735
QY 354 TMSIMKSCWWRADRPSPRELRLRLLEAAIKTADDEAV--LQVP 396
DB 736 ELYMLMRECWAHAPSQRPTFKQLVETLDRILATVAEEYLDLSMP 779

RESULT 6
TVHU2P
fibroblast growth factor receptor flg-2 precursor - human
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) flg-2
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
C:Accession: A60350; S21843
R:Avivi, A.; Zimmer, Y.; Yaron, A.; Yarden, Y.; Givol, D.
Oncogene 6, 1089-1092, 1991
A:Title: Flg-2, a new member of the family of fibroblast growth factor receptors.
A:Reference number: A60350; MUID:91296390; PMID:1648703
A:Accession: A60350
A:Molecule type: mRNA
A:Residues: 1-800 <AVI>
A:Cross-references: EMBL:X58255; NID:G31382; PIDN:CAA41209.1; PID:G31383
A:Experimental source: keratinocytes
C:Comment: This may be a receptor for keratinocyte growth factor.
C:Genetics:
A:Gene: GDB:FGFR2; JWS; CFD1; KGF; FLG2
A:Cross-references: GDB:127273; OMIM:176943
A:Map position: 10q25.3-10q26
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-800/Product: fibroblast growth factor receptor flg-2 #status predicted <MAT>
F:22-369/Domain: extracellular #status predicted <EXT>
F:131-137/Region: acidic
F:262-335/Domain: immunoglobulin homology <IMM>
F:370-390/Domain: transmembrane #status predicted <TMM>
F:391-800/Domain: intracellular #status predicted <INT>
F:464-749/Domain: protein kinase homology <KIN>
F:472-480/Region: protein kinase ATP-binding motif
F:59-107,170-222,269-333/Disulfide bonds: #status predicted
F:96-107,256,288,309,322/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:502,519,611/Active site: Lys, Glu, Asp #status predicted
F:616,629/Binding site: magnesium (Asn, Asp) #status predicted
F:642/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match      20.7%; Score 453.5; DB 1; Length 800;
Best Local Similarity 30.5%; Pred. No. 7.8e-16;
Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFLILGLVILWLFIREORTQOORSGPQGIAPV---PPPRDLSEWAGHGNVALPLKET 90
DB 375 VVFFELFVVAAILCLRLSPKGLGSPTVHKVSRFPLKRQVSLSSNMSNTPL--V 432
QY 91 SVENFLGATTPALA---KLQVP-----RQLSEVLEQICSGSGGPIFRANMTGD 137
DB 433 RIARLSSGEGEVLANVSELELPADPKWELSRTRLTLGKPLGEGCFGVWMAEATGIDKDR 492
QY 138 PSKPSVILKALKEPAGLHEVQDFLGRIOFQHYLGKHNVLQLEGCTCKPLMWLEDDV 197
DB 493 TAKEVTVAVMKDDATDKDLSLDVSEWEMMKMGKHNIIINLLGACTQGGFLVIVEYA 552
QY 198 AQGDLLGLFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLOEKHL 247
DB 553 AKGNLREFL--RARRP-----PGMDYSFDACRLPEQLTKDLVSCAYQVARGMEYLASKC 607
```

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSSTOT--IPLKWLAPERLLLRPASI 305
Db 608 IHRDLAARNVLVTEDNVNWKIADFGIARDVHNDIYKKTNGRLPDKVWMAPEALFDRVYTH 667
QY 306 RADVMSFGILLYEMVTLGAPPYVPEVPTSIHLQRRKIMKRPSSCTHTMYIMSKSCRW 365
Db 668 QSDVMSFGVLLWEIFTLGSGPYGIPVEELFKLLKEGHRMDKPSCTHDLVIMRECWHIA 727
QY 366 READRPSRELRLLE--AAIKTADDAVLQVP 396
Db 728 VPSQRTFKQLVEDLRLITVTSTDEYLDLSP 760

RESULT 7

A48991
heparin-binding growth factor receptor - mouse
N:Alternate names: HBGF receptor
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 04-Feb-2000
C:Accession: A48991
R:Katoch, O.; Hattori, Y.; Sasaki, H.; Sakamoto, H.; Fujimoto, K.; Fujii, T.; Sugimura, T.
Cancer Res. 53, 1136-1141, 1993
A:Title: Isolation of the complementary DNA encoding a mouse heparin-binding growth factor
A:Reference number: A48991; MUID:93177694; PMID:8382556
A:Accession: A48991
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-800 <KAT>
A:Cross-references: GB:S56291; NID:g298329; PIDN:AAB25535.1; PID:g298330
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBI:126536, NCBI:126537)
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein-
C:Keywords: ATP; growth factor receptor; heparin binding; phosphotransferase; tyrosine-
F:262-335/Domain: immunoglobulin homology <IMM>
F:464-749/Domain: protein kinase homology <KIN>
F:472-480/Region: protein kinase ATP-binding motif

Query Match 20.7%; Score 453.5; DB 2; Length 800;
Best Local Similarity 30.5%; Pred. No. 7.8e-16;
Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;
QY 34 VTIFILLLGVILWLFIREQRTQOORSGPOGIAPV---PPRDLSSWEAGHGNVALPLKET 90
Db 375 VVFFELVVAAILCLRLSPKPKGLGSPVTHKVSFFLKRQVLSNSSMNSNTPF--V 432
QY 91 SVENFLGATTPALA---KLQVP-----REQISEVLEQICSGSCGPIFRANNTGD 137
Db 433 RIARLSSGEGPVLNVSELEPADPKWLSRRLTLGKPLGEGCFQVVMMAEAGIDKDR 492
QY 138 PSKPKSVILKALKEPAGLHEVODFLGRIOHQVYLGKHNVLQLEGCTEKLPLYMVLVDV 197
Db 493 TAKPVTVAVMKLDATDKDLSLVSEMEMMKMGKHNIIINLLGACTQGGLPLYVEYA 552
QY 198 AQGDLIGLWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHL 247
Db 553 AKGNLREFL-RARRP-----PGMDYSFDACLPPEQLTKDLVSCAYQVARGMEYLASQKC 607
QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSSTOT--IPLKWLAPERLLLRPASI 305
Db 608 IHRDLAARNVLVTEDNVNWKIADFGIARDVHNDIYKKTNGRLPDKVWMAPEALFDRVYTH 667
QY 306 RADVMSFGILLYEMVTLGAPPYVPEVPTSIHLQRRKIMKRPSSCTHTMYIMSKSCRW 365
Db 668 QSDVMSFGVLLWEIFTLGSGPYGIPVEELFKLLKEGHRMDKPSCTHDLVIMRECWHIA 727
QY 366 READRPSRELRLLE--AAIKTADDAVLQVP 396
Db 728 VPSQRTFKQLVEDLRLITVTSTDEYLDLSP 760

RESULT 8

S38579

fibroblast growth factor receptor 3 - Iberian ribbed newt (fragment)
C:Species: Pleurodeles waltlil (Iberian ribbed newt)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S38579
R:Shi, D.L.; Fromentoux, V.; Launay, C.; Umbhauer, M.; Boucaut, J.C.
submitted to the EMBL Data Library, November 1993
A:Description: Expression of FGFR-3 in amphibian embryos.
A:Reference number: S38579
A:Accession: S38579
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-797 <SHI>
A:Cross-references: EMBL:X75603
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C:Keywords: ATP; growth factor receptor
F:258-331/Domain: immunoglobulin homology <IMM>
F:456-741/Domain: protein kinase homology <KIN>
F:464-472/Region: protein kinase ATP-binding motif

Query Match 20.4%; Score 447; DB 2; Length 797;
Best Local Similarity 28.8%; Pred. No. 1.6e-15;
Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;
QY 33 LVTFILLLGVILWLFIREQRTQOORSGPOGIAPVPPRDLSSWEAGHGNVALPL-KETS 91
Db 369 VAVVILVLIIFTYKMKPSSKKTMTATVHKVSKFPLKEQVLSNSSMNSNTPLVRIIR 428
QY 92 VENFLGATTPALAKLQVP-----REQISEVLEQICSGSCGPIFRANNTGDPSKP 141
Db 429 LSSDGPMLANVSELEPADPKWLSRRLTLGKPLGEGCFQVVMMAVAGIEKDKPNKA 488
QY 142 KSVILKALKEPAGLHEVODFLGRIOHQVYLGKHNVLQLEGCTEKLPLYMVLVDVACGD 201
Db 489 TSVAIVLKDDATDKDLSLVSEMEMMKMGKHNIIINLLGACTQGGLPLYVIVFVASKN 548
QY 202 LIGFLWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHLFHGD 251
Db 549 LREYL-RARRP-----PGMDYSFDTCPLPEQLTKDLVSCAYQVARGMEYLASQKCIHRD 603
QY 252 VAARNILMQSDLTAKLGLGLAYEYVTRGAISSSTOT--IPLKWLAPERLLLRPASI 309
Db 604 LAARNVLVTEDNVNWKIADFGIARDVHNDIYKKTNGRLPDKVWMAPEALFDRVYTHQSDV 663
QY 310 WSFGILLYEMVTLGAPPYVPEVPTSIHLQRRKIMKRPSSCTHTMYIMSKSCRWREAD 369
Db 664 WSFGVLLWEIFTLGSGPYGIPVEELFKLLKEGHRMDKPSCTHDLVIMRECWHAVPSQ 723

RESULT 9

A35963
protein-tyrosine kinase (BC 2.7.1.112) cek2 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Jul-1999
C:Accession: A35963
R:Pasquale, E.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990
A:Title: A distinctive family of embryonic protein-tyrosine kinase receptors.
A:Reference number: A35963; MUID:90332672; PMID:2165604
A:Accession: A35963
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-806 <PAS>
A:Cross-references: GB:M35195; NID:g211442; PIDN:AAA48664.1; PID:g211443
C:Genetics:
C:Gene: cek2
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor,
F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-806/Product: protein-tyrosine kinase cek2 #status predicted <MAT>
F:24-368/Domain: extracellular #status predicted <EXT>
F:131-138/Region: acidic

F:262-335/Domain: immunoglobulin homology <IMM>

F:369-389/Domain: transmembrane #status predicted <TM>

F:390-806/Domain: intracellular #status predicted <INT>

F:464-749/Domain: protein kinase homology <KIN>

F:472-480/Region: protein kinase ATP-binding motif

F:61-107, 170-222, 269-333/Disulfide bonds: #status predicted

F:96-219, 256, 288, 309, 322/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:502, 519, 611/Active site: Lys, Glu, Asp #status predicted

F:616, 629/Binding site: magnesium (Asn, Asp) #status predicted

F:642/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 20.4%; Score 446.5; DB 2; Length 806;
Best Local Similarity 30.1%; Pred No. 1.7e-15;
Matches 118; Conservative 79; Mismatches 164; Indels 31; Gaps 9;

Qy 31 TLLVTIFILGVILWLFIREQRTQQRSQPGIAPVPPR-DLSWEAGHGNGVALPL-K 88

Db 374 TGLVLFILVILVILICRMKPKAMNTTQKVSKEFLKQVSLSSNNSNTPLVR 433

Qy 89 ETSVENFICATTPALAKLQVP-----REQSLSEVLEQICSGSCGPIFRANMNTGDP 138

Db 434 ITRUSSGPMLANVSELEPPDKWELARGRLTLGKPLGEGCGVQVVMABEIGIDKDKP 493

Qy 139 SKPKSVILKALKEPAGLHEVODFLGRIOFHVGLGKHKNLVOLGCGCTEKLPLYMVLEDA 198

Db 494 NKAITVAVKMKDDATDKDLSLVSEMMKMGKHKNIINLLGACTGGPLVILVEYAS 553

Qy 199 QGDLGLGLFWTCRRDVMTMGGLY-----DLTEKQVYHIGKQVLLALEFLQEKLH 248

Db 554 KGNLREYL-RARRP-----PGMDYSFDCTKLPPEQLTFKDLVSCAYQVARGMEYLASQKI 608

Qy 249 HGDVVAARNILMQSDLTAKLGLGLAYEYVTRGAISSQT--IPLKWLAPERLLLRPASIR 306

Db 609 HRDLAARNVLVTEEDNMVKIADFLGARDVHNIIDYKKTNGRLPVKMWAPALFDRVYTHQ 668

Qy 307 ADVMSFGILLYEMVTGLAPPYEPVPTSLHLOQRKIMKRPSSCTHTMYSMKSCWR 366

Db 669 SDVWSFGVLLWEITFLGSGPPGIPVEELFKLLKEGHRMDPANCTHLYMIMRECWHAV 728

Qy 367 EADRPSPRELRLRLAEAI-KTADDEAV-LQVP 396

Db 729 PSQRPTFKQLVEDLDRVLTMTSTDEYLDLSP 760

RESULT 10
155363
fibroblast growth factor receptor 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: 155363; B53627
E:Ornitz, D.M.; Leder, P.
J. Biol. Chem. 267, 16305-16311, 1992
A:Title: Ligand specificity and heparin dependence of fibroblast growth factor receptors
A:Reference number: 155363; MUID:92355591; PMID:1379594
A:Accession: 155363
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-801 <RES>
A:Cross-references: GB:M81342; NID:g199144; PIDN:AAA39535.1; PID:g199145
R:Chellaiah, A.T.; McEwen, D.G.; Werner, S.; Xu, J.; Ornitz, D.M.
J. Biol. Chem. 269, 11620-11627, 1994
A:Title: Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in immunoglobulin heavy chain enhancer of 3' transcription (IGHV3-3) gene
A:Reference number: A53627; MUID:94209351; PMID:7512569
A:Accession: B53627
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 242-364 <CHE>
A:Cross-references: GB:L26492
C:Genetics:
A:Gene: mPR3

A;Introns: 304/3; 353/1
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; growth factor receptor
F:262-335/Domain: immunoglobulin homology <IMM>
F:464-750/Domain: protein kinase homology <KIN>
F:472-480/Region: protein kinase ATP-binding motif

Query Match 20.3%; Score 444; DB 2; Length 801;
Best Local Similarity 30.5%; Pred. No. 2.3e-15;

Matches 120; Conservative 71; Mismatches 165; Indels 38; Gaps 10;

Qy 34 VTIFILILGVILWLFIREQRTQQRSQPGIAPV---PPRDLSEWAGHGNGVALPLKET 90

Db 375 VVFFILVVAAILCRLRSPKGLGSPTHVKYSRFPKQVSLSSNNSNTPL--V 432

Qy 91 SVENFLGATTPALA---KLQVP-----REQSLSEVLEQICSGSCGPIFRANMNTGD 137

Db 433 RIARLSGEGFVLANVSELEPPDKWELSRTRLTGKPLGEGCGVQVVMABEIGIDKDR 492

Qy 138 PSKPSVILKALKEPAGLHEVODFLGRIOFHVGLGKHKNLVOLGCGCTEKLPLYMVLEDA 197

Db 493 TAKPVTVAVKMKDDATDKDLSLVSEMMKMGKHKNIINLLGACTGGPLVILVEY 552

Qy 198 AQGDLGLGLFWTCRRDVMTMGGLY-----DLTEKQVYHIGKQVLLALEFLQEKLH 247

Db 553 AKGNLREYL-RARRP-----PGMDYSFDACRLPEQLTKDLVSCAYQVARGMEYLASQKC 607

Qy 248 FHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSQT--IPLKWLAPERLLLRPAS 305

Db 608 IHRDLAARNVLVTEEDNMVKIADFLGARDVHNIIDYKKTNGRLPVKMWAPALFDRVYTH 667

Qy 306 RADVMSFGILLYEMVTGLAP--PYEPVPTSLHLOQRKIMKRPSSCTHTMYSMKSCWR 364

Db 668 QSDVWSFGVLLWEITFGGSPYEGIPVEELFKLLKEGHRMDPANCTHLYMIMRECWH 727

Qy 365 WREADRPSPRELRLRLAE--AAIKTADDEAVLQVP 396

Db 728 AVPSQRPTFKQLVEDLDRVLTMTSTDEYLDLSP 761

RESULT 11
TVHUF3

fibroblast growth factor receptor 3 precursor - human
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C:Accession: A38576; A55273; E38269; I51880

R:Keegan, K.; Johnson, D.E.; Williams, L.T.; Hayman, M.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 1095-1099, 1991

A:Title: Isolation of an additional member of the fibroblast growth factor receptor fami

A:Reference number: A38576; MUID:91142118; PMID:1847508

A:Accession: A38576

A:Molecule type: mRNA

A:Residues: 1-806 <KEE>

R:Cross-references: GB:M58051; NID:g182568; PIDN:AAA52450.1; PID:g182569

R:Thompson, L.M.; Plummer, S.; Schalling, M.; Altherr, M.R.; Gusella, J.F.; Housman, D.E

Genomics 11, 1133-1142, 1991

A:Title: A gene encoding a fibroblast growth factor receptor isolated from the Huntington

A:Reference number: A55273; MUID:92147110; PMID:1664411

A:Accession: A55273

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 76-394, 'V', 396-806 <THO>

A:Cross-references: GB:M64347; NID:g182564; PIDN:AAA58470.1; PID:g182565

A>Note: sequence extracted from NCBI backbone (NCBIP:80296)

R:Partanen, J.; Mäkelä, T.P.; Alitalo, R.; Lehtvaeslaiho, H.; Alitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A:Reference number: A38268; MUID:91062389; PMID:2247464

A:Accession: E38269

A:Molecule type: mRNA

A:Residues: 619-675 <PAR>

A:Cross-references: GB:M37782

R;Bellus, G.A.; Hefferon, T.W.; Ortiz de Luna, R.I.; Hecht, J.T.; Horton, W.A.; Machado, Am. J. Hum. Genet. 56, 368-373, 1995

A;Title: Achondroplasia is defined by recurrent G380R mutations of FGFR3.

A;Reference number: 151880; PMID:95150025; PMID:7847369

A;Accession: 151880

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 361-379, 'R', 381-415 <RES>

A;Cross-references: GB:S76733; NID:g914201; PIDN:AAB33323.1; PID:g914202

A;Note: this sequence represents a mutant form associated with achondroplasia

C;Genetics:

A;Gene: GDB:FGFR3

A;Cross-references: GDB:127526; OMIM:100800; OMIM:134934

A;Map position: 4p16.3-4p16.3

C;Function:

A;Description: receptor for both acidic and basic fibroblast growth factors

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-806/Product: fibroblast growth factor receptor 3 #status predicted <MAT>

F;23-375/Domain: extracellular #status predicted <EXT>

F;133-139/Region: acidic

F;268-341/Domain: immunoglobulin homology <IMM>

F;376-396/Domain: transmembrane #status predicted <TM>

F;397-806/Domain: intracellular #status predicted <INT>

F;470-755/Domain: protein kinase homology <KIN>

F;478-486/Region: protein kinase ATP-binding motif

F;61-109,176-228,275-339/Disulfide bonds: #status predicted

F;98,225,262,315,328/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;508,525,637/Active site: Lys, Glu, Asp #status predicted

F;622,635/Binding site: magnesium (Asn, Asp) #status predicted

F;648/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 20.3%; Score 444; DB 1; Length 806;

Best Local Similarity 30.5%; Pred. No. 2.3e-15;

Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

QY 34 VTIFILLLGVILWLFIREQRTQOQSGP---QGIAPVPPRLDSWEAGHGNNALPL-KE 89

DB 381 VGFFILVVAATVLCRLSPKGLGSPVTHKISRFFPKRQVLSNASMSNTPLVRI 440

QY 90 TSVENFLGATTPALAKLOVP-----REQLSEVLQICSGCGPIFRANMNTGDP 139

DB 441 ARLSGEGPTLANVSELEPADPKWELSRALTGLKPLGEGCGQVWAAEIGDKDRAA 500

QY 140 KPSVILKALKEPAGLHEVQDFLGRIOHYLKGKKNLVLEGGCTCKLPLYWVLEDAQ 199

DB 501 KPVTVAVKMLKDDATDKDLSDVSEMEMMKMTGKHKNIINLLGACTQGGPLVLYVEYAAK 560

QY 200 GDLGLFLWTCRRDVTMTDGLLY-----DLTEKQVYHTGKQVLLALEFLQEKHLFH 249

DB 561 GNLREFL-RARP-----PGLDYSFDTCKPPEQLTFKDLVSCAYQVARGMEYLAQKCIH 615

QY 250 GDAARNILMQSDTLAKLGLGLAYEVYTRGAISSTQT---IPKWLAPERLLLRPASTRA 307

DB 616 RDLAARNVLVTDNWKIADFGIARDVHNLDDYKKTNGRLPVKWKMAPEALDRVYTHQS 675

QY 308 DWWSGILLIYEMVTIGAPPYVPPTSTILEHIQRRKIMKRPSSCTHTWYSIMKSCWRWRE 367

DB 676 DWWSGVLLEWLTIGGSPYGPVVEELFKLKEGHRMDKPNCTHDLIMRECWHAP 735

QY 368 ADSPSPRLRLRLAIAIK-TADDE 390

DB 736 SQRPYFKQLVEDLRLVITVSTDE 759

RESULT 12

150128

fibroblast growth factor receptor - quail

C;Species: Coturnix coturnix (quail)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C;Accession: 150128; S42803

R;Marcelle, C.; Eichmann, A.; Halevy, O.; Breant, C.; Le Douarin, N.M.

Development 120, 683-694, 1994

A;Title: Distinct developmental expression of a new avian fibroblast growth factor recep

A;Reference number: 150128; PMID:94215505; PMID:8162862

A;Accession: 150128

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-713 <MAR>

A;Cross-references: EMBL:X76885; NID:g440139; PIDN:CAA54213.1; PID:g440140

C;Genetics:

A;Gene: FREX

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote

C;Keywords: ATP; growth factor receptor

F;176-247/Domain: immunoglobulin homology <IMM>

F;377-662/Domain: protein kinase homology <KIN>

F;385-393/Region: protein kinase ATP-binding motif

Query Match 20.1%; Score 439.5; DB 2; Length 713;

Best Local Similarity 29.0%; Pred. No. 3.5e-15;

Matches 131; Conservative 79; Mismatches 163; Indels 79; Gaps 15;

QY 21 EKQYEVILVPT---LLVTIFILLLGVILWLFIREQRTQOQSGPQGIAPV-----PP 69

DB 276 EAKYTDIIIIYSGSLAVAMALII--VVLC-----RMQTQSSKQPLPMAVHKLSKPL 326

QY 70 PRDLSWEAGHGNNALPLKETSVENFLGATTPALA-----KLQVPREQLSEVL- 117

DB 327 IRQFSLDSSSSGKSTSLMR--VTRLSSSCAPMLAGVVMEDLPDLSKWEPREKL--VLG 382

QY 118 PQICSGSGCPIFRANMNTGD---PSKPSVILKALKEPAGLHEVQDFLGRIOHYLGLKH 174

DB 383 KPLGEGCGQVVAEAYGIDRQWPDRAVTVAVKMLKDNATDKDLADLISEMEMMKLMOKH 442

QY 175 KNLVLEGGCTCKLPLYWVLEDAQDGLLGLFWTCRRDVTMTDGLLYDLTE-----K 226

DB 443 KMINILGVCTQDGLYVIVFAAKGNREYLRA--RRPPTD-YTFDITELHEBQLCK 499

QY 227 QVYHTGKQVLLALEFLQEKHLFHGDVAARNILMQSDTLAKLGLGLAYEVYTRGAISSTQ 286

DB 500 DLVSCVYQVARGMEYLESRRCIHRDLAARNVLVTAENWKIADFGIARDVHDIYVKTS 559

QY 287 T--IPKWLAPERLLLRPASTRADVWSFGILLIYEMVTIGAPPYVPPTSTILEHLQRRKI 344

DB 560 NGRLEPVKMAPEALDRVYTHQSDVWSFGILMWEIFTIGGSPYGPVVEELFKLKEGHR 619

QY 345 MKRPSSCTHTWYSIMKSCWRWREADRPSPRELRLLE---AAIK----- 385

DB 620 WDCPNCTHELIMRECWHAVLPQRPFKQLVEGLDKILAAISREYLDLSMPFEQYSPS 679

QY 386 -----TADDEAVLQVPELVVPELYAAVAG 409

DB 680 CEDTTSTCSDSDSVFTHDPMPLAPCLFSCPSG 711

RESULT 13

TVHUF4

fibroblast growth factor receptor 4 precursor - human

N;Alternate names: protein-tyrosine kinase tkf

N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C;Accession: S15345; A46615; A41598; D38269

R;Partanen, J.; Maekelae, T.P.; Eerola, E.; Korhonen, J.; Claesson-Welsh,

EMBO J. 10, 1347-1354, 1991

A;Title: FGFR-4, a novel acidic fibroblast growth factor receptor with a distinct expres

A;Reference number: S15345; PMID:91224085; PMID:1709094

A;Accession: S15345

A;Molecule type: mRNA

A;Residues: 1-802 <PAR>

A;Cross-references: EMBL:X57205; NID:g31371; PIDN:CAA40490.1; PID:g31372

A;Note: binds acidic but not basic fibroblast growth factor with high affinity

R;Ron, D.; Reich, R.; Chedid, M.; Lengel, C.; Cohen, O.E.; Chan, A.M.; Neufeld, G.; Mikl

J. Biol. Chem. 268, 5388-5394, 1993

A;Title: Fibroblast growth factor receptor 4 is a high affinity receptor for both acidic

Job time : 21 secs

```
QY 277 YTRGAISSTQTIPLKWLAPERILLRPSIRADVMSFGILLYEMVTLGAPPYEPVPTTIL 336
Db 544 TTNG-----RLPVKMAPEALFORVYTHQSDVMSFGVLMWEIFTLGSGSPGIPVEELF 597
QY 337 EHLQRRKIMKRPSSCTHMYSIMKSCWRREADRPSRELRLRLEAAIKTADDEAVLQVP 396
Db 598 KLLKEGHMDKPTNCTNELYMMRDCWHAVPQSQRFTFKQLVEDDLRLTLITNEEYLDLT 657
QY 397 E 397
Db 658 Q 658

RESULT 15
A38429
keratinocyte growth factor receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Jul-1999
C;Accession: A38429
R;Miki, T.; Fleming, T.P.; Bottaro, D.P.; Rubin, J.S.; Ron, D.; Aaronson, S.A.
Science 251, 72-75, 1991
A;Title: Expression cDNA cloning of the KGF receptor by creation of a transforming autoc
A;Reference number: A38429; MUID:91095977; PMID:1846048
A;Accession: A38429
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-707 <MIK>
A;Cross-references: GB:M33503; NID:g198593; PIDN:AAA39377.1; PID:g198594
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; autophosphorylation; growth factor receptor; phosphoprotein; transmembr
F;57-118/Domain: immunoglobulin homology <IMM>
F;365-650/Domain: protein kinase homology <KIN>
F;373-381/Region: protein kinase ATP-binding motif

Query Match 19.8%; Score 433; DB 2; Length 707;
Best Local Similarity 27.9%; Pred. No. 7.3e-15;
Matches 118; Conservative 84; Mismatches 165; Indels 56; Gaps 10;

QY 19 IQEKQYEVIIYPTLL-----VTILLILGLVILWLFIREQRTQQQSGPQGTIA----- 65
Db 250 VREK--EITASPDYLEIAIYICIGVFLIACMVVTVIFCRMKTTTKKDPFSSQPAVHKLTKR 307
QY 66 -PVPPPRDLISWAGHGNVALPLKETSVENFLGATTPALA-----KIQVPREQL 113
Db 308 IPLRQVTVSASSSSSMSNTPLVITTLSTADTFPLAGVSEYELPEDPKWEFPRDKL 367
QY 114 SEVLEQICSGSCGPIFRANMNTGDFSPKPK--SVILKALKEPAGLHEVQDFLGRIOFHQY 170
Db 368 T-LGKPLGEGCGQVVMAEAVGIDKDKPKAEVTVAVKMLKDDATEKDLSDLVSEMEMMKM 426
QY 171 LGKHKNLVQLEGCCCTEKLPLYMVLEDVAGDILLGLTLCRRDVTMDGLLYD----- 222
Db 427 IGKHKNIIINLGCATQDGLYVIVYASKGNREYLRRPFGMEYS---YDINRVPEEQ 483
QY 223 LTKQVYHIGKQVLLALFLQEKHLFPHGDVAARNILMQSDLTAKLCGLGLA-----Y 274
Db 484 MTFKDLVSTYQLARGMEVLAQKCIHRDLAARNVLVTENNVMKIADFGIARDINNIDYY 543
QY 275 EYVTRGALSSTQTIPLKWLAPERILLRPSIRADVMSFGILLYEMVTLGAPPYEPVPTT 334
Db 544 KKTING-----RLPVKMAPEALFDRVYTHQSDVMSFGVLMWEIFTLGSGSPGIPVEE 597
QY 335 ILEHLQRRKIMKRPSSCTHMYSIMKSCWRREADRPSRELRLRLEAAIKTADDEAVLIQ 394
Db 598 LFKLKEGHMDKPTNCTNELYMMRDCWHAVPQSQRFTFKQLVEDDLRLTLITNEEYLD 657
QY 395 VPE 397
Db 658 LTQ 660
```

Search completed: June 14, 2004, 18:46:17

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 18:45:49 ; Search time 48 Seconds
(without alignments)
2476.842 Million cell updates/sec

Title: US-10-040-884-3
Perfect score: 2192
Sequence: 1 MGMTMLLECSLSDKLCVIQ.....LYAAVAGIRVESLFYNSML 422

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2192	100.0	422	14	US-10-040-884-3
2	2188	99.8	458	15	US-10-240-145-67
3	1079	49.2	209	9	US-09-862-027-6
4	542	24.7	104	9	US-09-836-392-24
5	452	20.6	93	9	US-09-864-761-45860
6	444	20.3	806	12	US-10-403-161-58
7	444	20.3	806	15	US-10-394-322A-28
8	444	20.3	808	12	US-10-403-161-60
9	443	20.2	694	16	US-10-302-812-46
10	434	19.8	802	9	US-09-758-386-3
11	434	19.8	802	14	US-10-011-548-33
12	434	19.8	802	14	US-10-354-358-44
13	434	19.8	802	15	US-10-116-275-245
14	434	19.8	802	15	US-10-394-322A-29
15	434	19.8	802	16	US-10-302-812-48

16	432	19.7	822	10	US-09-757-415A-2	Sequence 2, Appli
17	427	19.5	821	15	US-10-394-322A-27	Sequence 27, Appli
18	427	19.5	821	16	US-10-302-812-44	Sequence 44, Appli
19	427	19.5	822	16	US-10-648-593-254	Sequence 254, App
20	424	19.3	735	12	US-10-307-817-6	Sequence 6, Appli
21	424	19.3	764	9	US-09-925-302-714	Sequence 714, App
22	424	19.3	764	12	US-09-925-302-714	Sequence 714, App
23	424	19.3	820	16	US-10-302-812-42	Sequence 42, Appli
24	424	19.3	822	12	US-10-307-817-8	Sequence 8, Appli
25	424	19.3	822	14	US-10-204-041-2	Sequence 2, Appli
26	424	19.3	822	15	US-10-394-322A-26	Sequence 26, Appli
27	424	19.3	824	12	US-10-307-817-4	Sequence 4, Appli
28	422	19.3	1130	14	US-10-204-041-4	Sequence 4, Appli
29	422	19.3	1148	12	US-10-170-385-181	Sequence 181, App
30	422	19.3	1148	16	US-10-408-765A-746	Sequence 746, App
31	421	19.2	650	12	US-10-403-847-116	Sequence 116, App
32	421	19.2	650	14	US-10-193-477-119	Sequence 119, App
33	420	19.2	394	12	US-10-087-192-1131	Sequence 1131, Ap
34	419	19.1	310	9	US-09-939-754-7	Sequence 7, Appli
35	419	19.1	310	9	US-09-939-832-7	Sequence 7, Appli
36	419	19.1	310	9	US-09-939-833-7	Sequence 7, Appli
37	419	19.1	887	15	US-10-258-666-8	Sequence 8, Appli
38	419	19.1	1567	14	US-10-312-918-2	Sequence 2, Appli
39	419	19.1	1594	14	US-10-312-918-4	Sequence 4, Appli
40	418.5	19.1	299	15	US-10-334-143-203	Sequence 203, App
41	417	19.0	1130	12	US-10-276-633-4	Sequence 4, Appli
42	417	19.0	1130	14	US-10-171-889-1	Sequence 1, Appli
43	417	19.0	1130	14	US-10-263-480-2	Sequence 2, Appli
44	417	19.0	1149	15	US-10-457-954-6	Sequence 6, Appli
45	415.5	19.0	891	9	US-09-862-027-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1

US-10-040-884-3
; Sequence 3, Application US/10040884
; Publication No. US2003007822A1
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE
; FILE REFERENCE: 70332/US Substantive
; CURRENT APPLICATION NUMBER: US/10/040,884
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US/09/310,438
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/088,958
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-040-884-3

Query Match 100.0%; Score 2192; DB 14; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.8e-190;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGMTMLLECSLSDKLCVIQEQYEVIIPTLLVTIFILLGLVILWLFIRQRTQQQRSG 60

Db 1 MGMTMLLECSLSDKLCVIQEQYEVIIPTLLVTIFILLGLVILWLFIRQRTQQQRSG 60

Qy 61 PQGLAPVPPRDLSWEAGHGNNVALPKETSVENFLGATTPALAKLQVPRQLSEVLQI 120

Db 61 PQGLAPVPPRDLSWEAGHGNNVALPKETSVENFLGATTPALAKLQVPRQLSEVLQI 120

Qy 121 CSGSCGPIFRANMTGDPSPKPSVILKALKEPAGLHEVQDFLGRIFQHYLGKHNVLQ 180

Db 121 CSGSCGPIFRANMTGDPSPKPSVILKALKEPAGLHEVQDFLGRIFQHYLGKHNVLQ 180

QY 181 EGCCTEKLPLYMWLEDAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
DB 181 EGCCTEKLPLYMWLEDAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
QY 241 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQTIPLKWLAPERLLL 300
DB 241 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQTIPLKWLAPERLLL 300
QY 301 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 360
DB 301 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 360
QY 361 SCWRWREADRPSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420
DB 361 SCWRWREADRPSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420
QY 421 ML 422
DB 421 ML 422

RESULT 2

US-10-240-145-67
; Sequence 67, Application US/10240145
; Publication No. US20030235883A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-048
; CURRENT APPLICATION NUMBER: US/10/240,145
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/668,680
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,618
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/728,711
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Custom
; SEQ ID NO 67
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-145-67

Query Match 99.8%; Score 2188; DB 15; Length 458;
Best Local Similarity 99.8%; Pred. No. 4.5e-190;
Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLLECSLSDKLCVIOEKQYEVLIIVPTLAVTIFLILGLVILWFIREQRTQOORSG 60
DB 37 MGMTMLLECSLSDKLCVIOEKQYEVLIIVPTLAVTIFLILGLVILWFIREQRTQOORSG 96
QY 61 PQGIAPVPPRDLSSWEAGHGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLEQI 120
DB 97 PQGIAPVPPRDLSSWEAGHGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLEQI 156
QY 121 CSGSCGPIFRANMNTGDPSPKPSVILKALKEPAGLHVQDFLGRIOFHQVILGHKNLVQL 180
DB 157 CSGSCGPIFRANMNTGDPSPKPSVILKALKEPAGLHVQDFLGRIRFHQVILGHKNLVQL 216
QY 181 EGCCTEKLPLYMWLEDAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
DB 217 EGCCTEKLPLYMWLEDAQDGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 276
QY 241 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQTIPLKWLAPERLLL 300

DB 277 FLQEKHLFHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQTIPLKWLAPERLLL 336
QY 301 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 360
DB 337 RPASTRADVWSFGILLIYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPSSCTHTWYSIMK 396
QY 361 SCWRWREADRPSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420
DB 397 SCWRWREADRPSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 456
QY 421 ML 422
DB 457 ML 458

RESULT 3

US-09-862-027-6
; Sequence 6, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: NO. US20020142428A1el Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-027-6

Query Match 49.2%; Score 1079; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 1e-89;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLGLGLA 273
DB 1 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLGLGLA 60
QY 274 YEVYTRGAISSTQTIPLKWLAPERLLLRLPASIRADVWSFGILLIYEMVTLGAPPYEVPPPT 333
DB 61 YEVYTRGAISSTQTIPLKWLAPERLLLRLPASIRADVWSFGILLIYEMVTLGAPPYEVPPPT 120
QY 334 SILEHLQRRKIMKRPSSCTHTWYSIMKSCWRWREADRPSPRELRLRLAAIKTADDEAVL 393
DB 121 SILEHLQRRKIMKRPSSCTHTWYSIMKSCWRWREADRPSPRELRLRLAAIKTADDEAVL 180
QY 394 QVPELVVPELYAAVAGIRVESLFYNSML 422
DB 181 QVPELVVPELYAAVAGIRVESLFYNSML 209

RESULT 4

US-09-836-392-24
; Sequence 24, Application US/09836392
; Patent No. US20020173458A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides,
; FILE REFERENCE: PT020P1
; CURRENT APPLICATION NUMBER: US/09/836,392
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US00/28066
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/159,542
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/165,914
; PRIOR FILING DATE: 1999-11-17

```
; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-392-24

Query Match      24.7%; Score 542; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5e-41;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 MVTIGAPVPEVPPTSILEHQRKIMKRPSSCTHTMYSIMKSCWRREADRPSRELRL 378
      |||||
Db 1 MVTIGAPVPEVPPTSILEHQRKIMKRPSSCTHTMYSIMKSCWRREADRPSRELRL 60

QY 379 RLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNSML 422
      |||||
Db 61 RLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNSML 104

RESULT 5
US-09-864-761-45860
; Sequence 45860, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
```

```
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45860
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021049.12
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EST HUMAN HIT: H08599.1, EVALUE 3.00e-05
; OTHER INFORMATION: SWISSPROT HIT: P77580, EVALUE 8.40e-01
US-09-864-761-45860

Query Match      20.6%; Score 452; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.3e-33;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 IAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQVPRQLSEVLEQICSG 123
      |||||
Db 1 IAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQVPRQLSEVLEQICSG 60

QY 124 SCGFIFRANMNTGDPSPKPSVILKALK 150
      |||||
Db 61 SCGFIFRANMNTGDPSPKPSVILKALK 87

RESULT 6
US-10-403-161-58
; Sequence 58, Application US/10403161
; Publication No. US2004004930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 58
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-58

Query Match      20.3%; Score 444; DB 12; Length 806;
Best Local Similarity 30.5%; Pred. No. 3.4e-31;
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;
```

```
QY 34 VTIFLLGLVILWLFIREFQRTQOORSGP---QGIAPVPPPPDLSSWAGHGNNVALPL-KE 89
Db 381 VGFLLFLLVAAVTLCLRLSPPKGLGSPVHKISRFPLKRVQSVLESNASMSNTPLVRI 440
QY 90 TSVENFLGATTALAKLOVP-----REQLSEVLEQICSGSCGPIFRANMNTGDPFS 139
Db 441 ARLSGEGPTLANVSELELPADPKWELSRARLTGKPLGEGCGFQVVMMAEAGIDKDRAA 500
QY 140 KPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQLEGCCCTEKLPLYMVLDEVAQ 199
Db 501 KPTVAVKMLKDDATDKDLSLVSEMMKMGKHNIIINLLGACTQGGGLYVLYVEYAAK 560
QY 200 GDLGLFWTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHLPH 249
Db 561 GNLREFL-RARRP----PGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQKCIH 615
QY 250 GDAARNILMQSDLTAKLGLGLAYEVYTRGAISSSTQT---IPLKWLAPERLLLRPASIRA 307
Db 616 RDLAARNVLVTEDNVNWKIADFGDLARDVHNDLYYKKTNGRLPVKWMAPALFDRVYTHQS 675

QY 308 DWMSFGILLYEMVTIGAPYEPVPPPTSILEHLORRKIMKRPSCTHTMYSIMKSCWRE 367
Db 676 DWMSFGVLLWEFTLGGSPYGPVBEELFKLKEGHRMDKPANCTHDLYMIMRECWAAP 735

QY 368 ADPSPRELRLRLAAIK-TADDE 390
Db 736 SQRPTEKQVLEDLDRVLVTWSTDE 759

RESULT 7
US-10-394-322A-28
; Sequence 28, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-28

Query Match 20.3%; Score 444; DB 15; Length 806;
Best Local Similarity 30.5%; Pred. No. 3.4e-31;
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

QY 34 VTIFLLGLVILWLFIREFQRTQOORSGP---QGIAPVPPPPDLSSWAGHGNNVALPL-KE 89
Db 381 VGFLLFLLVAAVTLCLRLSPPKGLGSPVHKISRFPLKRVQSVLESNASMSNTPLVRI 440
QY 90 TSVENFLGATTALAKLOVP-----REQLSEVLEQICSGSCGPIFRANMNTGDPFS 139
Db 441 ARLSGEGPTLANVSELELPADPKWELSRARLTGKPLGEGCGFQVVMMAEAGIDKDRAA 500
QY 140 KPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQLEGCCCTEKLPLYMVLDEVAQ 199
Db 501 KPTVAVKMLKDDATDKDLSLVSEMMKMGKHNIIINLLGACTQGGGLYVLYVEYAAK 560
QY 200 GDLGLFWTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHLPH 249
Db 561 GNLREFL-RARRP----PGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQKCIH 615
QY 250 GDAARNILMQSDLTAKLGLGLAYEVYTRGAISSSTQT---IPLKWLAPERLLLRPASIRA 307
Db 616 RDLAARNVLVTEDNVNWKIADFGDLARDVHNDLYYKKTNGRLPVKWMAPALFDRVYTHQS 675
```

```
QY 308 DWMSFGILLYEMVTIGAPYEPVPPPTSILEHLORRKIMKRPSCTHTMYSIMKSCWRE 367
Db 676 DWMSFGVLLWEFTLGGSPYGPVBEELFKLKEGHRMDKPANCTHDLYMIMRECWAAP 735

QY 368 ADPSPRELRLRLAAIK-TADDE 390
Db 736 SQRPTEKQVLEDLDRVLVTWSTDE 759

RESULT 8
US-10-403-161-60
; Sequence 60, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 60
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-60

Query Match 20.3%; Score 444; DB 12; Length 808;
Best Local Similarity 30.5%; Pred. No. 3.4e-31;
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

QY 34 VTIFLLGLVILWLFIREFQRTQOORSGP---QGIAPVPPPPDLSSWAGHGNNVALPL-KE 89
Db 381 VGFLLFLLVAAVTLCLRLSPPKGLGSPVHKISRFPLKRVQSVLESNASMSNTPLVRI 442
QY 90 TSVENFLGATTALAKLOVP-----REQLSEVLEQICSGSCGPIFRANMNTGDPFS 139
Db 441 ARLSGEGPTLANVSELELPADPKWELSRARLTGKPLGEGCGFQVVMMAEAGIDKDRAA 502
QY 140 KPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHNVLQLEGCCCTEKLPLYMVLDEVAQ 199
Db 503 KPTVAVKMLKDDATDKDLSLVSEMMKMGKHNIIINLLGACTQGGGLYVLYVEYAAK 562
QY 200 GDLGLFWTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHLPH 249
Db 563 GNLREFL-RARRP----PGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQKCIH 617
QY 250 GDAARNILMQSDLTAKLGLGLAYEVYTRGAISSSTQT---IPLKWLAPERLLLRPASIRA 307
Db 618 RDLAARNVLVTEDNVNWKIADFGDLARDVHNDLYYKKTNGRLPVKWMAPALFDRVYTHQS 677
```



```
QY 308 DVWSFGILLYEMVTGAPPEVPTSLIEHLQRRKIMKRPSSCTHTMYSIMKSCWRWRE 367
; DVWSFGILLYEMVTGAPPEVPTSLIEHLQRRKIMKRPSSCTHTMYSIMKSCWRWRE 367
Db 678 DVWSFGILLWEFTLGGSPYGPVPEELFKLLKEGHRMDKPANCHDLYMIMRECWAHP 737
; DVWSFGILLWEFTLGGSPYGPVPEELFKLLKEGHRMDKPANCHDLYMIMRECWAHP 737
QY 368 ADSPSPRELRLRLAAIK-TADDE 390
; ADSPSPRELRLRLAAIK-TADDE 390
Db 738 SORPTFKQLVEDLDRVLTVTSTDE 761
; SORPTFKQLVEDLDRVLTVTSTDE 761

RESULT 9
US-10-302-812-46
; Sequence 46, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND
; TISSUE REGENERATION
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-302-812-46

Query Match 20.2%; Score 443; DB 16; Length 694;
Best Local Similarity 30.7%; Pred. No. 3.4e-31;
Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

QY 44 ILWLFIREQRTQQORSQPGIAPVPPPRDLSEAGHGNVALPL-KETSVENFLGATTPA 102
; ILWLFIREQRTQQORSQPGIAPVPPPRDLSEAGHGNVALPL-KETSVENFLGATTPA 102
Db 285 IQWL--KHVEVNGSKVGDG-TPVTVLKVSLENAWSNTPLVRIARLSSGEGPTLAN 341
; KHVEVNGSKVGDG-TPVTVLKVSLENAWSNTPLVRIARLSSGEGPTLAN 341
QY 103 LAKLQVP-----REQLEVELEQICSGSCGPIFRANMNTGDPKSKSVILKALKEP 152
; LAKLQVP-----REQLEVELEQICSGSCGPIFRANMNTGDPKSKSVILKALKEP 152
Db 342 VSELELPADPKWELSRARLTGKPLGEGCFQVVMAEAGIDKRAAKPVTVAVKMLKDD 401
; VSELELPADPKWELSRARLTGKPLGEGCFQVVMAEAGIDKRAAKPVTVAVKMLKDD 401
QY 153 AGLHEVQDFLGRIOFHQVGLKHKLVQLEGCTEKLPLYMVLEDAVQDGLLGFLWTCRRD 212
; AGLHEVQDFLGRIOFHQVGLKHKLVQLEGCTEKLPLYMVLEDAVQDGLLGFLWTCRRD 212
Db 402 ATDKDLSLDVSEMEMMKMIGKHKNIINLLGACTQGGLYVLEVAAGNREFL-RARRP 460
; ATDKDLSLDVSEMEMMKMIGKHKNIINLLGACTQGGLYVLEVAAGNREFL-RARRP 460
QY 213 VMTMDGLLY-----DLTEKQVYHIGKOVLLALEFLQKHLFEGDVAARNILMQSD 262
; DLTEKQVYHIGKOVLLALEFLQKHLFEGDVAARNILMQSD 262
Db 461 ----PGLDYSFDCTKPEEQTLTKDLYSCAYQVARGMEYLAQKCIHRDLAARNVLVTE 516
; PGLDYSFDCTKPEEQTLTKDLYSCAYQVARGMEYLAQKCIHRDLAARNVLVTE 516
QY 263 LTAKLGLGLAYEYVYTRGAISSTQT--IPLKWLAPERILLRPAIRADVMSFGILLYEMV 320
; LTAKLGLGLAYEYVYTRGAISSTQT--IPLKWLAPERILLRPAIRADVMSFGILLYEMV 320
Db 517 NVMKIADFGIARDVHNLDDYKKTNGRLPVKMAPEALFDRVYTHQSDVMSFGVLLWEIF 576
; NVMKIADFGIARDVHNLDDYKKTNGRLPVKMAPEALFDRVYTHQSDVMSFGVLLWEIF 576
QY 321 TLGAPPYEVPTSLIEHLQRRKIMKRPSSCTHTMYSIMKSCWRWREADRPSRELRLRL 380
; TLGAPPYEVPTSLIEHLQRRKIMKRPSSCTHTMYSIMKSCWRWREADRPSRELRLRL 380
Db 577 TLGSPYPGIPVEELFKLLKEGHRMDKPANCHDLYMIMRECWAHPSPQRTFKQLVEDL 636
; TLGSPYPGIPVEELFKLLKEGHRMDKPANCHDLYMIMRECWAHPSPQRTFKQLVEDL 636
QY 381 EAAIK-TADDE 390
; EAAIK-TADDE 390
Db 637 DRVLTVTSTDE 647
; DRVLTVTSTDE 647

RESULT 10
US-09-758-386-3
; Sequence 3, Application US/09758386
; Patent No. US20010016335A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-5
; FILE REFERENCE: PF486PCT
; CURRENT APPLICATION NUMBER: US/09/758,386
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/293,152
; PRIOR FILING DATE: 1999-04-16
```

```
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-386-3

Query Match 19.8%; Score 434; DB 9; Length 802;
Best Local Similarity 29.8%; Pred. No. 2.7e-30;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQYEVIIV---PTLLVTIFILILGVTILWLFIREQRTQQORSQP-----OGIAPVPPPRDL 73
; EKQYEVIIV---PTLLVTIFILILGVTILWLFIREQRTQQORSQP-----OGIAPVPPPRDL 73
Db 364 EARTDILLYASGSLAAVLLLAGL-----YRQALHGRHPRPPATVQKLSRFLARQF 418
; EARTDILLYASGSLAAVLLLAGL-----YRQALHGRHPRPPATVQKLSRFLARQF 418
QY 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125
; SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125
Db 419 SLESGSGKSSSLVRGVRLLSSGPPALLAGLVSLDLPLDPLWEPRDRRLVLGKPLGEGCF 478
; SLESGSGKSSSLVRGVRLLSSGPPALLAGLVSLDLPLDPLWEPRDRRLVLGKPLGEGCF 478
QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIOFHQVGLKHKLVQLEG 182
; GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIOFHQVGLKHKLVQLEG 182
Db 479 GOVVRAEAFGMDFARPDPQASTVAVMKLNKASDKDLADLVSEMEVMKLIIGRHKNIINLLG 538
; GOVVRAEAFGMDFARPDPQASTVAVMKLNKASDKDLADLVSEMEVMKLIIGRHKNIINLLG 538
QY 183 CTEKPLPLYMVLEDAVQDGLLGFLWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232
; CTEKPLPLYMVLEDAVQDGLLGFLWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQEGPLYVIVECAAGNREFL-RARRPPGPDLSPPGPRSSGGLSPFVLVSCAY--- 594
; VCTQEGPLYVIVECAAGNREFL-RARRPPGPDLSPPGPRSSGGLSPFVLVSCAY--- 594
QY 233 KQVLLALEFLQKHLFEGDVAARNILMQSDITAKLGLGLAYEYVYTRGAISSTQT--IPL 290
; KQVLLALEFLQKHLFEGDVAARNILMQSDITAKLGLGLAYEYVYTRGAISSTQT--IPL 290
Db 595 -QVARGMQYLESRKCIHRDLAARNVLVTEEDNMKIDFGLARGVHHIDYKKTNGRLPV 653
; -QVARGMQYLESRKCIHRDLAARNVLVTEEDNMKIDFGLARGVHHIDYKKTNGRLPV 653
QY 291 KWLAPERILLRPAIRADVMSFGILLYEMVTGAPPEVPTSLIEHLQRRKIMKRPSS 350
; KWLAPERILLRPAIRADVMSFGILLYEMVTGAPPEVPTSLIEHLQRRKIMKRPSS 350
Db 654 KMWAPALFDRVYTHQSDVMSFGILLWEIFTLGSGPYPGIPVEELFKLLKEGHRMDRPPH 713
; KMWAPALFDRVYTHQSDVMSFGILLWEIFTLGSGPYPGIPVEELFKLLKEGHRMDRPPH 713
QY 351 CTHMTYIMKSCWRWREADRPSRELRLRLAAIKTADDE 390
; CTHMTYIMKSCWRWREADRPSRELRLRLAAIKTADDE 390
Db 714 CPPELYGLMRECWAHPSPQRTFKQLVEDLKVLLAVSEE 753
; CPPELYGLMRECWAHPSPQRTFKQLVEDLKVLLAVSEE 753

RESULT 11
US-10-548-33
; Sequence 33, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; Debets, Johannes Eduard Maria
; Antonius
; Sana, Theodore R.
; Bazan, J. Fernando
; Kaselein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
; Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,548
; FILING DATE: 22-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/173,151
```

```

; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030055218A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-011-548-33

Query Match          19.8%; Score 434; DB 14; Length 802;
Best Local Similarity 29.8%; Pred. No. 2.7e-30;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQEVILV---PTLLVTFILLLGVILWLFIREQTQOORSGP-----QGIAPVPPRDL 73
Db 364 EARYTDIILYASGSLALAVLLLAGL-----YRQALHGRHPRPATVQKLSRFFLARQF 418

QY 74 SWEAGHGNNALPL-KETSVENFLGATTPALAKLOVPREQLSE-----VL-EQICSGSC 125
Db 419 SLESGSSGKSSSLVGVVRLSSGALLAGLSLDPLDPLWEFDRDLVLGKPLGEGCF 478

QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRHQYVGLKHNVLQLEG 182
Db 479 GQVRAEAFGMDPARPDQASTAVAKMLKDNASDKDLADLVSEMVKMLIGRHKNIINLLG 538

QY 183 CTEKPLPLYMVLVEDVAQDGLLGFLWTCRDV---MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQEGPLYVIVECAKGNLREFL-RARRPPGPDLSPDGPRSGEGLSPFVLVSCAY--- 594

QY 233 KOVLLALEPQLQKHLFHGVDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT--IPL 290
Db 595 -QVARGMQYLESKKCIHRDLAARNVLVTEEDNVKMTADFGLAGRVHHIDYKKTSNGRLPV 653

QY 291 KWLAPERILLRPASTRADVWMSFGILLYEMVTIGAPPYEPVPTTSILEHLQRRKIMKRPS 350
Db 654 KWMPEALFDRVYTHQSDVWMSFGILLWEIFTLGGSPYGPVPEELFSLRLREGHRMDRPPH 713

QY 351 CTHMTYSIMKSCWRWREADRPSRELRLLEAAIKTADDE 390
Db 714 CPPELYGLMRECWAHAPSQRPTFKQLVEALDKVLLAVSEE 753

RESULT 12
US-10-354-358-44
; Sequence 44, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea

```

```

; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 58862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MPI02-020PIRNMNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-44

Query Match          19.8%; Score 434; DB 14; Length 802;
Best Local Similarity 29.8%; Pred. No. 2.7e-30;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQEVILV---PTLLVTFILLLGVILWLFIREQTQOORSGP-----QGIAPVPPRDL 73
Db 364 EARYTDIILYASGSLALAVLLLAGL-----YRQALHGRHPRPATVQKLSRFFLARQF 418

QY 74 SWEAGHGNNALPL-KETSVENFLGATTPALAKLOVPREQLSE-----VL-EQICSGSC 125
Db 419 SLESGSSGKSSSLVGVVRLSSGALLAGLSLDPLDPLWEFDRDLVLGKPLGEGCF 478

QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRHQYVGLKHNVLQLEG 182
Db 479 GQVRAEAFGMDPARPDQASTAVAKMLKDNASDKDLADLVSEMVKMLIGRHKNIINLLG 538

QY 183 CTEKPLPLYMVLVEDVAQDGLLGFLWTCRDV---MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQEGPLYVIVECAKGNLREFL-RARRPPGPDLSPDGPRSGEGLSPFVLVSCAY--- 594

QY 233 KOVLLALEPQLQKHLFHGVDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT--IPL 290
Db 595 -QVARGMQYLESKKCIHRDLAARNVLVTEEDNVKMTADFGLAGRVHHIDYKKTSNGRLPV 653

QY 291 KWLAPERILLRPASTRADVWMSFGILLYEMVTIGAPPYEPVPTTSILEHLQRRKIMKRPS 350
Db 654 KWMPEALFDRVYTHQSDVWMSFGILLWEIFTLGGSPYGPVPEELFSLRLREGHRMDRPPH 713

QY 351 CTHMTYSIMKSCWRWREADRPSRELRLLEAAIKTADDE 390

```

Db 714 CPPELYGLMRECWAAPSQRPTFKOLVEALDKVLLAVSEE 753

RESULT 13

US-10-116-275-245

Sequence 245, Application US/10116275

Publication No. US20030211476A1

GENERAL INFORMATION:

APPLICANT: Elan Pharmaceutical Technology

APPLICANT: O'Mahony, Daniel J.

APPLICANT: Brayden, David

APPLICANT: Byrne, Daragh

APPLICANT: Lambkin, Imelda

APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and

FILE REFERENCE: E1067/20087

CURRENT APPLICATION NUMBER: US/10/116,275

CURRENT FILING DATE: 2002-10-04

NUMBER OF SEQ ID NOS: 349

SOFTWARE: PatentIn version 3.1

SEQ ID NO 245

LENGTH: 802

TYPE: PRT

ORGANISM: Homo sapiens

US-10-116-275-245

Query Match 19.8%; Score 434; DB 15; Length 802;

Best Local Similarity 29.8%; Pred. No. 2.7e-30;

Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQYEVIIV---PTLLVTFILGLVILWLFIREQRTQQORSQP---QGIAPVPPRDL 73

Db 364 EARYTDIILYASGSLAVLALLAGL-----YRQALHGRHPRPATVQKLSRFLARQF 418

QY 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125

Db 419 SLESGSGKSSSLVRGVRLLSSGFPALLAGLVSLDPLDPLWEFFPRDRILVGLKPLGEGCF 478

QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIOHQHVLGKHKNLVQLEG 182

Db 479 GQVRAEAFGMDPARPDQAQSTAVVRKMDNADSKDLADLVSEMEVMKILGRHKNILNIG 538

QY 183 CTEKLPLYMWLEDAQGDLLGLFWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232

Db 539 VCTQEGPLYVIVECAKGNLREFL-RARRPPGPDLSPOGPRSSGEPFLSFFVLVSCAY--- 594

QY 233 KOVLLALEFLOEKHLFHGDVAARNILMOSDLTAKLGLGLAYEVYTRGAISSQT--IPL 290

Db 595 -QVARGMQLSRSKCIHRDLAARNVLVTDNVMKIADFLARGVHHIDYKKTNSGRLPV 653

QY 291 KWLAPERLLRPASIRADVWSFGILLYEMVTLGAPPYEVPTSTILEHLQRRKIMKRPS 350

Db 654 KWAPEALFDRVYTHQSDVWSFGILLWEIFTLGGSPYGPVPEELFSLREGHRMDRPPH 713

QY 351 CTHMYSIMKSCWRREADRPSRELRLLEAAIKTADDE 390

Db 714 CPPELYGLMRECWAAPSQRPTFKOLVEALDKVLLAVSEE 753

RESULT 14

US-10-394-322A-29

Sequence 29, Application US/10394322A

Publication No. US20030232391A1

GENERAL INFORMATION:

APPLICANT: SUNESIS PHARMACEUTICALS, INC.

APPLICANT: Prescott, John C.

TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS

FILE REFERENCE: 39750-0006 US

CURRENT APPLICATION NUMBER: US/10/394,322A

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: US 60/366,892

PRIOR FILING DATE: 2002-03-21

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29

; LENGTH: 802

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-394-322A-29

Query Match 19.8%; Score 434; DB 15; Length 802;

Best Local Similarity 29.8%; Pred. No. 2.7e-30;

Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQYEVIIV---PTLLVTFILGLVILWLFIREQRTQQORSQP---QGIAPVPPRDL 73

Db 364 EARYTDIILYASGSLAVLALLAGL-----YRQALHGRHPRPATVQKLSRFLARQF 418

QY 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125

Db 419 SLESGSGKSSSLVRGVRLLSSGFPALLAGLVSLDPLDPLWEFFPRDRILVGLKPLGEGCF 478

QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIOHQHVLGKHKNLVQLEG 182

Db 479 GQVRAEAFGMDPARPDQAQSTAVVRKMDNADSKDLADLVSEMEVMKILGRHKNILNIG 538

QY 183 CTEKLPLYMWLEDAQGDLLGLFWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232

Db 539 VCTQEGPLYVIVECAKGNLREFL-RARRPPGPDLSPOGPRSSGEPFLSFFVLVSCAY--- 594

QY 233 KOVLLALEFLOEKHLFHGDVAARNILMOSDLTAKLGLGLAYEVYTRGAISSQT--IPL 290

Db 595 -QVARGMQLSRSKCIHRDLAARNVLVTDNVMKIADFLARGVHHIDYKKTNSGRLPV 653

QY 291 KWLAPERLLRPASIRADVWSFGILLYEMVTLGAPPYEVPTSTILEHLQRRKIMKRPS 350

Db 654 KWAPEALFDRVYTHQSDVWSFGILLWEIFTLGGSPYGPVPEELFSLREGHRMDRPPH 713

QY 351 CTHMYSIMKSCWRREADRPSRELRLLEAAIKTADDE 390

Db 714 CPPELYGLMRECWAAPSQRPTFKOLVEALDKVLLAVSEE 753

RESULT 15

US-10-302-812-48

Sequence 48, Application US/10302812

Publication No. US20040087016A1

GENERAL INFORMATION:

APPLICANT: Keating et al.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND

FILE REFERENCE: HYDR-P02-004

CURRENT APPLICATION NUMBER: US/10/302,812

CURRENT FILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn version 3.1

SEQ ID NO 48

LENGTH: 802

TYPE: PRT

ORGANISM: Homo sapiens

US-10-302-812-48

Query Match 19.8%; Score 434; DB 16; Length 802;

Best Local Similarity 29.8%; Pred. No. 2.7e-30;

Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQYEVIIV---PTLLVTFILGLVILWLFIREQRTQQORSQP---QGIAPVPPRDL 73

Db 364 EARYTDIILYASGSLAVLALLAGL-----YRQALHGRHPRPATVQKLSRFLARQF 418

QY 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLQVPREQLSE-----VL-EQICSGSC 125

Db 419 SLESGSGKSSSLVRGVRLLSSGFPALLAGLVSLDPLDPLWEFFPRDRILVGLKPLGEGCF 478

QY 126 GPIFRANMNTGDPKSP---KSVILKALKEPAGLHEVQDFLGRIOHQHVLGKHKNLVQLEG 182

Db 479 GOVZAEAFGMDPARPDQASTVAVXMKDNASDKDLADLVSEMEVWKLGRHKNIINLLG 538
QY 183 CTEKLPYMWLEDAQGDLLGFLWTCRRDV---MTMDG-----LLYDLTEKQVYHIG 232
Db 539 VCTQEGPLYVIVECAAKGNLREFL-RARRPPGDLSPDGRSSEGPLSPPLVSCAY--- 594
QY 233 KOVLLALEFLOEKHLFHGDAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT--IPL 290
Db 595 -QVARGMOYLESKCIHRDLAARNVLVTEDNVMKIADFGARGVHHIDYKKTSNGRLPV 653
QY 291 KWLAPERILLRPAISRADVWVSGILLIYEMVTLGAPPYEPVPTSIIEHLQRRKIMKRPSS 350
Db 654 KWAPEALFDRVYTHQSDVWSFGILLWEIFTLGGSPYGPVPEELFSLREGHRMDRPH 713
QY 351 CHTHTMYSIMKSWRWREADRPSPRELRLLEAAIKTADDE 390
Db 714 CPPELYGLMRECWAAPSQRPTFKQVLEALDKVLLAVSEE 753

Search completed: June 14, 2004, 18:51:43
Job time : 50 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 18:43:09 ; Search time 22 Seconds
(without alignments)
990.280 Million cell updates/sec

Title: US-10-040-884-3

Perfect score: 2192

Sequence: 1 MGMTMLLECSLKDLCVIQ.....LYAAVAGIRVESLFYNSML 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1079	49.2	209	4	US-09-345-473E-6
2	444	20.3	801	3	US-09-383-630-6
3	444	20.3	806	3	US-09-383-630-3
4	435	19.8	310	2	US-08-701-191A-8
5	435	19.8	310	4	US-09-664-526-8
6	434.5	19.8	378	1	US-08-070-165F-8
7	434.5	19.8	378	2	US-08-885-418-8
8	434	19.8	802	4	US-03-173-151A-33
9	433	19.8	652	1	US-08-471-570-10
10	427	19.5	821	2	US-08-451-822A-13
11	427	19.5	821	4	US-08-323-430-13
12	424	19.3	729	1	US-07-640-029-3
13	424	19.3	731	1	US-07-921-807B-5
14	424	19.3	731	1	US-08-441-944A-5
15	424	19.3	731	3	US-08-439-992A-3
16	424	19.3	733	1	US-07-640-029-4
17	424	19.3	733	1	US-07-921-807B-6
18	424	19.3	733	1	US-08-441-944A-6
19	424	19.3	733	3	US-08-439-992A-4
20	424	19.3	820	1	US-07-921-807B-3
21	424	19.3	820	1	US-08-441-944A-3
22	424	19.3	820	3	US-08-439-992A-1
23	424	19.3	822	1	US-07-997-133-1
24	424	19.3	822	1	US-07-921-807B-4
25	424	19.3	822	1	US-08-441-944A-4
26	424	19.3	822	2	US-08-451-822A-12
27	424	19.3	822	3	US-08-439-992A-2

```

28      424      19.3      822      4      US-08-323-430-12      Sequence 12, Appl
29      423.5      19.3      820      1      US-08-166-717D-6      Sequence 6, Appli
30      423      19.3      769      1      US-08-471-570-8      Sequence 8, Appli
31      422.5      19.3      816      1      US-07-640-029-1      Sequence 1, Appli
32      422      19.3      822      1      US-08-459-296-2      Sequence 2, Appli
33      419      19.1      310      2      US-08-701-191A-1      Sequence 1, Appli
34      419      19.1      310      2      US-08-701-191A-6      Sequence 6, Appli
35      419      19.1      310      4      US-09-390-326-7      Sequence 7, Appli
36      419      19.1      310      4      US-09-664-526-1      Sequence 1, Appli
37      419      19.1      310      4      US-09-664-526-6      Sequence 6, Appli
38      419      19.1      315      2      US-08-701-191A-2      Sequence 2, Appli
39      419      19.1      315      4      US-09-664-526-2      Sequence 3, Appli
40      419      19.1      351      2      US-08-701-191A-3      Sequence 3, Appli
41      419      19.1      351      4      US-09-664-526-3      Sequence 3, Appli
42      418.5      19.1      299      2      US-08-701-191A-13      Sequence 13, Appl
43      418.5      19.1      299      4      US-09-664-526-13      Sequence 13, Appl
44      418.5      19.1      300      2      US-08-701-191A-31      Sequence 31, Appl
45      418.5      19.1      300      4      US-09-664-526-31      Sequence 31, Appl

```

ALIGNMENTS

RESULT 1

US-09-345-473E-6

; Sequence 6, Application US/09345473E

; Patent No. 6558903

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin

; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof

; FILE REFERENCE: 35800/183781

; CURRENT APPLICATION NUMBER: US/09/345,473E

; CURRENT FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-345-473E-6

Query Match 49.2%; Score 1079; DB 4; Length 209;

Best Local Similarity 100.0%; Pred. No. 8.2e-91;

Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      214      MTMDGLYDITEKQVYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLGLGLA 273
Db      1      MTMDGLYDITEKQVYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLGLGLA 60

QY      274      YEVYTRGAISSSTOTPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPPT 333
Db      61      YEVYTRGAISSSTOTPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPPT 120

QY      334      SILFHLQRRKIMKRPSSCTTHMYSIMKSCWRWRADRPSPRELRLLEAAIKTADDEAVL 393
Db      121      SILFHLQRRKIMKRPSSCTTHMYSIMKSCWRWRADRPSPRELRLLEAAIKTADDEAVL 180

QY      394      QVPELVVPELYAAVAGIRVESLFYNSML 422
Db      181      QVPELVVPELYAAVAGIRVESLFYNSML 209

```

RESULT 2

US-09-383-630-6

; Sequence 6, Application US/09383630A

; Patent No. 6265632

; GENERAL INFORMATION:

; APPLICANT: Avner Yayon et al.

; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH

; FACTOR RECEPTOR ASSOCIATED

; CHONDRODYSPLASIA

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
to an ASCII file

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A

Filing DATE: 26-Aug-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 1402/2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 801

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-383-630-6

Query Match 20.3%; Score 444; DB 3; Length 801;

Best Local Similarity 30.5%; Pred. No. 5.6e-32;

Matches 120; Conservative 71; Mismatches 165; Indels 38; Gaps 10;

QY 34 VTIFLLGVILWLFIREQRTQQRSGPGIAPV---PPRDLSEAGHGNVALPLKET 90

DB 375 VVFFILVVAATLCRLSPKPKGLSGPTVHKVSRFPLKQVLSNESMSNSTPL--V 432

QY 91 SVENFLGATTPALA---KLQVP-----REQLSEVLEQICSGSCGPIFRANMTGD 137

DB 433 RIARLSSGEGPVLAVNSELELPADPKWELSRRLTLGKPLGEGCGQVVMARAIQDKDR 492

QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIQFHOVLGKHKNLVLEGGCTEKLPLYMVLVDV 197

DB 493 TAKPVTVAVKMLKDDATDKDLSLVSEMEMMKMIGKHKNIIINLGNCTGGPLVLYVEYA 552

QY 199 AGCDLIGFWLTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHL 247

DB 553 AKGNLREFL--RARRP---PGMDYSFDACKLPEEQTLTKDLVSCAYQVARGMEYLASQKC 607

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSTQT--IPLKWLAPERLLRPASTI 305

DB 608 IIRDLAARNVLVTEDNVNMIADFGIARDVHNLDDYKKTNGRLPVKMAPEALFORVYTH 667

QY 306 RADVMSFGILLYEMVTLGAP--PYPEVPPTSILEHLQRRKIMKRPSSCTHTMYSIMKSCWR 364

DB 668 QSDVMSFGVLLWEIFFPGSPVPYGPVPEELFKLLKEGHRMDKPACTHDLVIMRECWH 727

QY 365 WREADRPSPRELRLIE--AAIKTADDEAVLQVP 396

DB 728 AVFSORPTPKQLVEDLRLITVTSTDEYLDLSVP 761

RESULT 3

US-09-383-630-3

; Sequence 3, Application US/09383630A

Patent No. 6265632
GENERAL INFORMATION:
APPLICANT: Avner Yayon et al.
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
CHONDRODYSPLASIA

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 2001 Jefferson Davis Highway, Suite 207

CITY: Arlington

STATE: Virginia

COUNTRY: United States of America

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 6.2,

Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted

to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/383,630A

FILING DATE: 26-Aug-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 1402/2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 806

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-383-630-3

Query Match 20.3%; Score 444; DB 3; Length 806;

Best Local Similarity 30.5%; Pred. No. 5.7e-32;

Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

QY 34 VTIFLLGVILWLFIREQRTQQRSGP---QGIAPVPPRDLSEAGHGNVALPL-KE 89

DB 381 VGFFILVVAATLCRLSPKPKGLSGPTVHKISRFPKQVLSNESMSNSTPLVRI 440

QY 90 TSVENFLGATTPALAKLQVP-----REQLSEVLEQICSGSCGPIFRANMTGDPS 139

DB 441 ARLSGEGPVLAVNSELELPADPKWELSRRLTLGKPLGEGCGQVVMARAIQDKRAA 500

QY 140 KPSVILKALKEPAGLHEVQDFLGRIQFHOVLGKHKNLVLEGGCTEKLPLYMVLVDVAQ 199

DB 501 KEPTVAVKMLKDDATDKDLSLVSEMEMMKMIGKHKNIIINLGNCTGGPLVLYVEYAAK 560

QY 200 GDLGLFWLTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHLPH 249

DB 561 GNLREFL--RARRP---PGLDYSFDTCPEPEQLTKDLVSCAYQVARGMEYLASQKCIH 615

QY 250 GDVAARNILMQSDLTAKLGLGLAYEYVTRGAISSTQT--IPLKWLAPERLLRPASTI 307

DB 616 RDLAARNVLVTEDNVNMIADFGIARDVHNLDDYKKTNGRLPVKMAPEALDRVYTHQS 675

QY 308 DVMSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKRPSSCTHTMYSIMKSCWRRE 367

DB 676 DVMSFGVLLWEIFFTGGSPYGPVPEELFKLLKEGHRMDKPACTHDLVIMRECWHAAAP 735

QY 368 ADPSPRELRLLEAAIK-TADDE 390
 Db 736 SORPTFKQLVEDLDRVLTSTDE 759

RESULT 4

US-08-701-191A-8
 ; Sequence 8, Application US/08701191A
 ; Patent No. 5942428
 ; GENERAL INFORMATION:
 ; APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
 ; and Stevan R. Hubbard
 ; TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
 ; OF NON-INSULIN RECEPTOR TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 41
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Fast-Seq for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/701,191A
 ; FILING DATE: August 21, 1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 227/088
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 310 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-701-191A-8

Query Match 19.8%; Score 435; DB 2; Length 310;
 Best Local Similarity 33.4%; Pred. No. 1e-31;
 Matches 102; Conservative 62; Mismatches 121; Indels 20; Gaps 6;
 QY 101 PALAKLVPREQLS--EVLEQICSGSCGPIFRANMNTGDPKPKSVILKALKEPAGLHEV 158
 Db 11 PADPKWLSRARLTGLKPLGEGCGQVVMABEAGIDKDRRAKPVTVAVKMLKDDATDKDL 70
 QY 159 QDFLGRIOFHQYLGKHNKLVLEGCCCTEKLPLYMVLEDAQDGLLGFMTCCRDVMTMDG 218
 Db 71 SDLVSEMEMMKWIGKHNNIINLLGACTGGGLYVLVEYAAKGNLREFL-RARRP----PG 125
 QY 219 LLY-----DLTEKQVYHIGKQVLLALEFLQEKHLPHGDAARNILMQSDLTAKLC 268
 Db 126 LDYSFDTCKPPEEQLTGKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLTEDNVKIA 185
 QY 269 GLGLAYEVYTRGAISSQT--IPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPP 326
 Db 186 DFGIARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVMSFGVLLWEIFTLGGSP 245

QY 327 YPEVPPTSILEHLQRRKIMKRPSSCTHTMYSIMKSCWRWREADRPSRELRLLEAAIK- 395
 Db 246 YPGIPVEELFKLLKEGHRMDKPNCTHDLYMIRECWMHAAPSQRPTFKQLVEDLDRVLT 305

QY 386 TADDE 390
 Db 306 TSTDE 310

RESULT 5

US-09-664-526-8
 ; Sequence 8, Application US/09664526
 ; Patent No. 6682921
 ; GENERAL INFORMATION:
 ; APPLICANT: MOHAMMADI, MOOSA
 ; APPLICANT: SCHLESSINGER, JOSEPH
 ; APPLICANT: HUBBARD, STEVAN R.
 ; TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
 ; RECEPTOR TYROSINE KINASES
 ; FILE REFERENCE: 038602/0847
 ; CURRENT APPLICATION NUMBER: US/09/664,526
 ; CURRENT FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: 09/188,809
 ; PRIOR FILING DATE: 1998-11-09
 ; PRIOR APPLICATION NUMBER: 08/701,191
 ; PRIOR FILING DATE: 1996-08-21
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 310
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-664-526-8

Query Match 19.8%; Score 435; DB 4; Length 310;
 Best Local Similarity 33.4%; Pred. No. 1e-31;
 Matches 102; Conservative 62; Mismatches 121; Indels 20; Gaps 6;
 QY 101 PALAKLVPREQLS--EVLEQICSGSCGPIFRANMNTGDPKPKSVILKALKEPAGLHEV 158
 Db 11 PADPKWLSRARLTGLKPLGEGCGQVVMABEAGIDKDRRAKPVTVAVKMLKDDATDKDL 70
 QY 159 QDFLGRIOFHQYLGKHNKLVLEGCCCTEKLPLYMVLEDAQDGLLGFMTCCRDVMTMDG 218
 Db 71 SDLVSEMEMMKWIGKHNNIINLLGACTGGGLYVLVEYAAKGNLREFL-RARRP----PG 125
 QY 219 LLY-----DLTEKQVYHIGKQVLLALEFLQEKHLPHGDAARNILMQSDLTAKLC 268
 Db 126 LDYSFDTCKPPEEQLTGKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLTEDNVKIA 185
 QY 269 GLGLAYEVYTRGAISSQT--IPLKWLAPERLLLRPASIRADVMSFGILLYEMVTLGAPP 326
 Db 186 DFGIARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVMSFGVLLWEIFTLGGSP 245
 QY 327 YPEVPPTSILEHLQRRKIMKRPSSCTHTMYSIMKSCWRWREADRPSRELRLLEAAIK- 385
 Db 246 YPGIPVEELFKLLKEGHRMDKPNCTHDLYMIRECWMHAAPSQRPTFKQLVEDLDRVLT 305
 QY 386 TADDE 390
 Db 306 TSTDE 310

RESULT 6

US-08-070-165F-8
 ; Sequence 8, Application US/08070165F
 ; Patent No. 5750365
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiu, Ing-Ming
 ; APPLICANT: Poulin, Matthew L
 ; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:

ZIP: 43210

OPERATING SYSTEM: PC-DOS/MS-DOS

COUNTRY: USA
ZTD: 43210


```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173,151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/095,987
; FILING DATE: 10-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-173-151A-33

```

```

Query Match      19.8%; Score 434; DB 4; Length 802;
Best Local Similarity 29.8%; Pred. No. 4.6e-31;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

```

```

Qy 21 EKQVEIIV--PTLLVTFILILGVILWLFIREQTOQQRSGP-----QGIAPVPPPRDL 73
Db 364 EARYTDIILYAGSLAVALLLAGL-----YRQALHGRHPRPATVQKLSRFLARQF 418

Qy 74 SWEAGHGNVALPL-KETSVENFLGATTPALAKLOVPREQLSE-----VL-EOICSGSC 125
Db 419 SLESGSGKSSSLVRGVRLSSGFALLAGLVSLDPLDPLWEFPDRDLVLGKPLGEGCF 478

Qy 126 GPIFRANMNTGDPSPK---KSVILKALKEPAGLHEVQDFLGRIOFHOVLGKHK 182
Db 479 GOVVRARAFGMDPARPDQASTAVAKMLKDNASDKDLADLVSEMEVMKLIHRHKNILNLG 538

Qy 183 CCTKRLPLYMVLVDVAQDGLGLFWLTCRRDV---MTMDG-----LLYDLTERQVYHIG 232
Db 539 VCTQEGPLYVIVECAAKGNLREFL-RARRPPGPDLSPPGSRSSGCLSPFLVLSVAY--- 594

Qy 233 KOVLLALEFLQEKHLFGHDVAARNILMQSDUTAKLCGLGLAYEVYTRGAISSTQT--IPL 290
Db 595 -QVARGMQYLESRKCIHRDLAARNVLVTEDNVMKIADFLARGVHHIDYKKTSNGRLPV 653

Qy 291 KWLAPERLLLPASTRADVWSFGILLYEMVTILGAPPYEVVPTSLFHLQRRKTMKRPSS 350
Db 654 KWAPEALFDRVYTHQSDVWSFGILLMEIFITGSGSPYPIGVSELFSLREGHRMDRPPH 713

Qy 351 CTHWTYIMKSCWRWREADSPRELRLRLAAIKTADDE 390
Db 714 CPPELYGLMRCWHAAPSQRPTFKQVLEALDKVLLAVSEE 753

```

RESULT 9

```

US-08-471-570-10
; Sequence 10, Application US/08471570
; Patent No. 5750371
; GENERAL INFORMATION:
; APPLICANT: IGARASHI, Koichi
; APPLICANT: SENOO, Masaharu
; APPLICANT: WATANABE, Tatsuya
; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,570
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,664
; FILING DATE:
; APPLICATION NUMBER: US 07/743369
; FILING DATE: 16-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: LINEK, Ernest V
; REGISTRATION NUMBER: 29822
; REFERENCE/DOCKET NUMBER: 40897
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 652 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-570-10

```

```

Query Match      19.8%; Score 433; DB 1; Length 652;
Best Local Similarity 28.0%; Pred. No. 4.3e-31;
Matches 115; Conservative 82; Mismatches 162; Indels 52; Gaps 9;

```

```

Qy 22 KQYEVIIPTLL-----VTFILILGVILWLFIREQTO-----QQQRSGPQGIAPVPP 69
Db 251 REKEITASPDYLEIATYICIGVFLIACMVTVILCRMKNITKKPDFSQPAVHKLTKRPL 310

Qy 70 PRDLSWAGHGNVALPLKETSVENFLGATTPALA-----KLOVPREQLSEVLE 118
Db 311 RRQVSASSSSMSNTPFLVITRITLSSTADTPMLAGVSEYELPDPKPWEPRDKLT-IGK 369

Qy 119 QICSGSGCPIFRANMNTGDPSPK---SVILKALKEPAGLHEVQDFLGRIOFHOVLGKHK 175
Db 370 PLGSGCGQVVMFAEAVGIDKDKPEAVTVAVKMLKDDATEKDLSDLVSEMEMMKMIKHK 429

Qy 176 NLVLEGCCTEKPLPLYMVLVDVAQDGLGLFWLTCRRDVTMDGLLYD-----LTEKQ 227
Db 430 NIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYS---YDINRVPEEQMTFKD 486

Qy 228 VYHIGKQVLLALEFLQEKHLFGHDVAARNILMQSDUTAKLCGLGLA-----YEVYTR 279
Db 487 LVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFLGARDINNIIDYKKTTN 546

Qy 280 GAISSTQTIPLKWLAPERLLLPASTRADVWSFGILLYEMVTILGAPPYEVVPTSLILEHL 339

```

QY 117 LEICSGSCGPIFRANMNTGDPKPK--SVILKALKEPAGLHEVQDFLGRIQHFHVLGK 173

QY 22 QKEYIIVPTLL-----VTFLILLGVILWLFIREQTQQRSGPOGIA-----PV 67

Qy	147	KALKEPAGLHEVQDFLGRIOFHQYLGKHKNLVOLFEGCCTEKIPLYMVLVEDVAQGDLLGFL	206
Db	423	KWLKSDATEKDLSDLISEWEMWKMIGKHNIINLLGACTQDGPLYIVIVEYASKGNREYL	482
Qy	207	WTCRRDVTMDGLLY-----DLTEKQVYHIGKQVLLALEFLOEKHLFHGDDVAARN	256
Db	483	QARR-----PPGLECYNPNPESHPEQLSSKDILVSCAYQVARGMEYLASKKCIHRDLAARN	537
Qy	257	ILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWLAPERLLLRPASIRADVWSFGI	314
Db	538	VLVTEDNMVKIADFLGARDIHHIDYKYKTTNGRLEVKWMAPEALFDRIYTHQSDVWSEGV	597
Qy	315	LLYEMVTILGAPPYEPVPPTSILEHLQRRKIMKRPSSTHTMYSIMKSCWRWREADRPSPR	374
Db	598	LLWEIFTLGGSPYGPVPVEELFKLLKEGHRMDKPSNCTNELYMMNRDCWHAVPSORPTEK	657
Qy	375	ELRLLEAAIKTADDEAVIQV	395
Db	658	QLVEDLDRIVALTSNQEYLDL	678

Search completed: June 14, 2004, 18:46:52
Job time : 23 secs

This Page Blank (uspto)

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	2192	100.0	422	3	RAY44297	RAY44297	Human rec
2	2192	100.0	495	4	AAB65706	AAB65706	Novel pro
3	2189	99.9	422	3	RAY44299	RAY44299	Human rec
4	2188	99.8	458	4	AAU68537	AAU68537	Human nov
5	2183	99.6	422	4	AAG66404	AAG66404	Human fib
6	2176.5	99.3	421	3	RAY44298	RAY44298	Human rec
7	1079	49.2	209	4	AAB66603	AAB66603	Human h14
8	743	33.9	183	4	AAE65707	AAE65707	Human pro
9	542	24.7	104	4	AAE00672	AAE00672	Human pro
10	452	20.6	93	4	ABB43239	ABB43239	Peptide #
11	452	20.6	93	4	AAW37079	AAW37079	Peptide #
12	452	20.6	93	4	AAW76972	AAW76972	Human bon
13	452	20.6	93	4	AAW64146	AAW64146	Human bra
14	452	20.6	93	4	ABG58633	ABG58633	Human liv
15	444	20.3	801	4	AAE21977	AAE21977	Mouse fib
16	444	20.3	806	4	AAE21976	AAE21976	Human fib
17	444	20.3	806	6	ABJ38646	ABJ38646	FGFR3 pro
18	444	20.3	806	6	ADA89050	ADA89050	Human FGF
19	444	20.3	806	6	AAE36462	AAE36462	Human FGF
20	443	20.2	694	5	ABG66739	ABG66739	Human nov
21	435	19.8	652	2	AAE15269	AAE15269	Clone pTB
22	435	19.8	687	2	AAW06456	AAW06456	FGF198-FG
23	434.5	19.8	378	2	AAW37805	AAW37805	Fibroblas
24	434.5	19.8	378	2	AAW23632	AAW23632	Newt fib
25	434	19.8	802	5	AAE16588	AAE16588	Human fib

Tue Jun 15 09:35:26 2004

us-10-040-884-3.rag

inflammatory pelvic disease; multiple sclerosis; psoriasis.

KW New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.
 XX cancers for treating adenocarcinoma.
 OS Claim 11; Page 49-50; 56pp; English.
 XX The present sequence is a human receptor tyrosine kinase (RTK) which
 CC activates Cdc2 kinase that mediates mitosis. Tyrosine kinase is
 CC selectively expressed in human forebrain. It is overexpressed in large
 CC number of carcinomas (e.g. adenocarcinoma) and brain tissues of Alzheimer
 CC patients. Dominant negative mutants derived from the RTK act as tyrosine
 CC kinase modulators. The sequence is used to identify compounds that
 CC modulate biological and/or pharmacological activity of tyrosine kinase
 CC and hence regulate cellular and tissue physiology. The present sequence
 CC and the modulators of tyrosine kinase are used for treating many diseases
 CC related to or mediated by RTK e.g. adenocarcinomas, angiogenesis,
 CC arthritis, diabetic retinopathy, ischaemic heart disease,
 CC atherosclerosis, inflammation, solid tumours and metastases
 XX
 SQ Sequence 422 AA;
 Query Match 100.0%; Score 2192; DB 3; Length 422;
 Best Local Similarity 100.0%; Pred. No. 8.2e-215;
 Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILWFIREQTOOQSG 60
 Db 1 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILWFIREQTOOQSG 60
 QY 61 PQGIAPVPPRDLISWEAGHGNVALPKETSVENFLGATTPALAKLQVPEQLSEVLEQI 120
 Db 61 PQGIAPVPPRDLISWEAGHGNVALPKETSVENFLGATTPALAKLQVPEQLSEVLEQI 120
 QY 121 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 180
 Db 121 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 180
 QY 181 EGCCTEKLPLYMWLEDAQGLLGFIMWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 Db 181 EGCCTEKLPLYMWLEDAQGLLGFIMWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 QY 241 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 300
 Db 241 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 300
 QY 301 RPASIRADVWSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 360
 Db 301 RPASIRADVWSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 360
 QY 361 SCWRREADRPSRELRLRLAAIKTADDEAVIQVPELVPELYAAVAGIRVESLIFYNYS 420
 Db 361 SCWRREADRPSRELRLRLAAIKTADDEAVIQVPELVPELYAAVAGIRVESLIFYNYS 420
 QY 421 ML 422
 Db 421 ML 422
 RESULT 2
 AAB65706
 ID AAB65706 standard; protein; 495 AA.
 XX
 AC AAB65706;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase, SEQ ID NO: 235.
 XX
 XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; infertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW

KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 XX Homo sapiens.
 XX WO200073469-A2.
 XX 07-DEC-2000.
 XX 26-MAY-2000; 2000WO-US014842.
 XX 28-MAY-1999; 99US-0136503P.
 XX (SUGE-) SUGEN INC.
 XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
 XX WPI; 2001-032161/04.
 XX N-PSDB; AAF44735.
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 XX treating immune-related diseases and disorders, cardiovascular disease,
 XX neurodegenerative diseases and/or cancers.
 XX Claim 10; Fig 1; 310pp; English.
 XX The present sequence is a novel protein kinase. The novel protein kinases
 XX and the nucleic acids that encode them may be used in the treatment and
 XX diagnosis of diseases associated with inappropriate kinase expression
 XX such as immune-related diseases and disorders, cardiovascular disease,
 XX neurodegenerative diseases and/or cancers. The nucleic acids and
 XX complementary sequences may also be used as DNA probes in diagnostic
 XX assays. The kinase polypeptides may be used as antigens in the production
 XX of antibodies of kinase expression and activity. Anti-kinase antibodies
 XX and kinase antagonists may also be used to down regulate kinase
 XX expression and activity. Diseases related to kinase expression and
 XX activity include rheumatoid arthritis, atherosclerosis, autoimmune
 XX disorders, complications of organ transplantation, myocardial infarction,
 XX immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
 XX stress related disorders, chronic inflammatory bowel disease, chronic
 XX inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 XX psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
 XX disorders
 XX
 SQ Sequence 495 AA;
 Query Match 100.0%; Score 2192; DB 4; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1e-214;
 Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILWFIREQTOOQSG 60
 Db 74 MGTRMLLECSLSDKLCVIOEKQYEVIIPTLLVTIFLLGLVILWFIREQTOOQSG 133
 QY 61 PQGIAPVPPRDLISWEAGHGNVALPKETSVENFLGATTPALAKLQVPEQLSEVLEQI 120
 Db 134 PQGIAPVPPRDLISWEAGHGNVALPKETSVENFLGATTPALAKLQVPEQLSEVLEQI 193
 QY 121 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 180
 Db 194 CSGSGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOPHQYLGKHKNLVQL 253
 QY 181 EGCCTEKLPLYMWLEDAQGLLGFIMWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 Db 254 EGCCTEKLPLYMWLEDAQGLLGFIMWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 313
 QY 241 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 300
 Db 314 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTPIPLKWLAPERLLL 373
 QY 301 RPASIRADVWSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 360
 Db 374 RPASIRADVWSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPSSCTHTMYSIMK 433

QY 361 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 420
 Db 434 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 493
 QY 421 ML 422
 Db 494 ML 495

RESULT 3
 ID AAY44299 standard; protein; 422 AA.
 AC AAY44299;
 XX 29-FEB-2000 (first entry)
 DT Human receptor tyrosine kinase dominant negative mutant-2.
 DE Human; receptor tyrosine kinase; RTK; tyrosine kinase modulator;
 XX signal transduction tyrosine kinase; tumour; dominant negative mutant;
 KW cancer; adenocarcinoma; RTK associated disorder; adenocarcinoma;
 KW angiogenesis; arthritis; diabetic retinopathy; ischaemic heart disease;
 KW atherosclerosis; inflammation.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FH Misc-difference 147 /note="Wild type Lys substituted by Arg"
 FT
 XX
 PN WO9964589-A1.
 PD 16-DEC-1999.
 XX
 PF 08-JUN-1999; 99WO-GB001798.
 XX
 PR 11-JUN-1998; 98US-0088958P.
 XX
 PA (ZONE) ZENECA LTD.
 XX
 PI Ghildyal N, Panchamoorthy G;
 XX WPI; 2000-097538/08.
 DR
 XX New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.
 PT cancers for treating adenocarcinoma.
 PT
 PS Claim 4; Page; 56pp; English.
 XX
 CC The present sequence is a dominant negative mutant of human receptor
 CC tyrosine kinase (RTK), which is obtained by substituting wild type Lys at
 CC position 147 with Arg. The mutant modulates biological and/or
 CC pharmacological activity of tyrosine kinase and hence regulates cellular
 CC and tissue physiology. The present sequence is used for treating many
 CC diseases related to or mediated by RTK e.g. adenocarcinomas,
 CC angiogenesis, arthritis, diabetic retinopathy, ischaemic heart disease,
 CC atherosclerosis, inflammation, solid tumours and metastases. Note: The
 CC present sequence is not given in the specification but has been derived
 CC from SEQ ID NO: 3 given in Sequence Listing
 XX
 SQ Sequence 422 AA;

Query Match 99.9%; Score 2189; DB 3; Length 422;
 Best Local Similarity 99.8%; Pred. No. 1.7e-214;
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLLECSLSKLCVIOKEQYEVIVPTLLVTFILLLGVILWLFIREQRTQQQRS 60
 Db 1 MGMTMLLECSLSKLCVIOKEQYEVIVPTLLVTFILLLGVILWLFIREQRTQQQRS 60
 QY 61 PQGIAPVPPPRDLSWEAGHGNNVALPLKETSVENFLGATTPALAKLQVPRQLSEVLEQI 120

Db 61 PQGIAPVPPPRDLSWEAGHGNNVALPLKETSVENFLGATTPALAKLQVPRQLSEVLEQI 120
 QY 121 CSGSCGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHKNLVQL 180
 Db 121 CSGSCGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHKNLVQL 180
 QY 181 EGCCTEKLPLYMVLDEVAQGDLLGFLWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 Db 181 EGCCTEKLPLYMVLDEVAQGDLLGFLWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 QY 241 FLOEKHLFEGDVAARNILMQSDLTAKLCGLIAYEYVTRGAISSQTOTIPLKWLAPERLLL 300
 Db 241 FLOEKHLFEGDVAARNILMQSDLTAKLCGLIAYEYVTRGAISSQTOTIPLKWLAPERLLL 300
 QY 301 RPASIRADVMSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPSCTHTMTSIMG 360
 Db 301 RPASIRADVMSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMKRPSCTHTMTSIMG 360
 QY 361 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 420
 Db 361 SCWRREADRPSPRELRLLEAAIKTADDEAVLQVPELVPELYAAVAGIRVESLFYNYS 420
 QY 421 ML 422
 Db 421 ML 422

RESULT 4
 AAU68537
 ID AAU68537 standard; protein; 458 AA.
 XX AAU68537;
 XX 16-JAN-2002 (first entry)
 XX Human novel cytokine encoded by cDNA 790CIP2C_8 #1.
 DE
 XX Human; cytokine; cell proliferation; cell differentiation;
 KW antinflammatory; stem cell growth factor; activin; inhibin; cancer;
 KW nervous system disease; neuropathy; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; spinal cord disorder;
 KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
 KW platelet disorder; thrombocytopaenia; stem cell disorder;
 KW aplastic anaemia; tissue regeneration; wound healing; ulcer;
 KW osteoporosis; osteoarthritis; bone degenerative disorder;
 KW periodontal disease; fibrosis; reperfusion; immune disorder;
 KW severe combined immunodeficiency; infection; autoimmune disorder;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;
 KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;
 KW inflammatory bowel disease; food supplement; immunogen.
 XX
 OS Homo sapiens.
 OS WO200175093-A1.
 PN 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US010484.
 XX 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PR 22-SEP-2000; 2000US-00668680.
 PR 23-OCT-2000; 2000US-00695618.
 PR 30-NOV-2000; 2000US-00728711.
 PR 14-MAR-2001; 2001US-00808701.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 XX Xu C, Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C;
 PI Drmanac RT;
 XX

DR WPI; 2001-626432/72.
 DR N-PSDB; AAS59829.
 XX New polypeptides and nucleic acids, useful for diagnosis, treatment of
 PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
 PT degenerative disorders, cancer and promoting wound healing.
 XX Claim 20; Page 261; 336pp; English.
 XX The invention relates to isolated human polypeptides (which may be
 CC cytokines) and the polynucleotides encoding them. The protein is useful
 CC for identifying a compound which binds to it (e.g. modulators, agonists
 CC and antagonists). The polynucleotides are useful as an array for mismatch
 CC detection. The proteins and nucleic acids are useful as nutritional
 CC sources or supplements. The protein exhibits exhibits activity relating
 CC to cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity, immune stimulating or immune
 CC suppressing and activin or inhibin related activities. The proteins (and
 CC antibodies raised against them) and nucleic acids are therefore useful in
 CC the diagnosis and treatment of diseases and disorders such as cancer,
 CC central and peripheral nervous system diseases and neuropathies,
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular
 CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,
 CC thrombocytopaenia, stem cell disorders, aplastic anaemia, for
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, and in tissue repair, healing of burns, incisions, ulcers, or
 CC treating osteoporosis, osteoarthritis, bone degenerative disorders, or
 CC periodontal disease, lung or liver fibrosis, reperfusion injury in
 CC various tissues, various immune deficiencies and disorders including
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
 CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes mellitus, myasthenia gravis), allergic reactions and conditions,
 CC such as asthma or other respiratory problems, coagulation disorders,
 CC haemophilia, septic shock, sepsis, arthritis, nephritis and inflammatory
 CC bowel disease, viral infection and are useful in altering bodily
 CC characteristics. The present sequence represents a novel protein of the
 CC invention
 XX
 SQ Sequence 458 AA;
 Query Match 99.8%; Score 2186; DB 4; Length 458;
 Best Local Similarity 99.8%; Pred. No. 2.4e-214;
 Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGMTMLLECSLSKLCVIOEQVEVIIVPTLLVTFILLLGVILWLFIREQTOOQSG 60
 Db 37 MGMTMLLECSLSKLCVIOEQVEVIIVPTLLVTFILLLGVILWLFIREQTOOQSG 96
 QY 61 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 120
 Db 97 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 156
 QY 121 CSGSGGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHYLGKHNVLVL 180
 Db 157 CSGSGGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHYLGKHNVLVL 216
 QY 181 EGCCTEKLPLYMVLVEDVAQGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 Db 217 EGCCTEKLPLYMVLVEDVAQGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 276
 QY 241 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 300
 Db 277 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 336
 QY 301 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTSIHLQRRKMKRPSSCTHTMYSIMK 360
 Db 337 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTSIHLQRRKMKRPSSCTHTMYSIMK 396
 QY 361 SCWRREADRSPRELRLRLAAIKTADDEAVLQVPELVVPELVVPELVVPELVVPELVVPELVV 420
 Db 397 SCWRREADRSPRELRLRLAAIKTADDEAVLQVPELVVPELVVPELVVPELVVPELVVPELVV 456

QY 421 ML 422
 Db 457 ML 458
 RESULT 5
 AAG66404
 ID AAG66404 standard; protein; 422 AA.
 XX
 AC AAG66404;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Human fibrous growth factor receptor 46.
 XX
 KW Human; fibrous growth factor receptor 46; cancer; HIV infection;
 KW cytostatic; anti-HIV.
 XX
 OS Homo sapiens.
 XX
 PN CN1296965-A.
 XX
 PD 30-MAY-2001.
 XX
 PF 23-NOV-1999; 99CN-00124072.
 XX
 PR 23-NOV-1999; 99CN-00124072.
 XX
 PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-483896/53.
 N-PSDB; AAH75803.
 XX
 XX Polypeptide-human fibrous growth factor receptor 46 and polynucleotide
 PT for coding said polypeptide.
 XX
 PS Claim 1; Page 22-23 (Disclosure); 29pp; Chinese.
 XX
 CC The present sequence is the protein sequence for human fibrous growth
 CC factor receptor 46. The receptor and its coding sequence are useful in
 CC the treatment of diseases e.g. cancer and HIV infection
 CC
 SQ Sequence 422 AA;
 Query Match 99.6%; Score 2183; DB 4; Length 422;
 Best Local Similarity 99.5%; Pred. No. 6.8e-214;
 Matches 420; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGMTMLLECSLSKLCVIOEQVEVIIVPTLLVTFILLLGVILWLFIREQTOOQSG 60
 Db 1 MGMTMLLECSLSKLCVIOEQVEVIIVPTLLVTFILLLGVILWLFIREQTOOQSG 60
 QY 61 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 120
 Db 61 PQGIAPVPPRDLISWEAGHGNVALPLKETSVENFLGATTAPALAKLOVPREQLSEVLEQI 120
 QY 121 CSGSGGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHYLGKHNVLVL 180
 Db 121 CSGSGGPIFRANMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHYLGKHNVLVL 180
 QY 181 EGCCTEKLPLYMVLVEDVAQGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 Db 181 EGCCTEKLPLYMVLVEDVAQGLLGLFWTCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 QY 241 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 300
 Db 241 FLOEKHLPHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSQTQIPLKWLAPERLLL 300
 QY 301 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTSIHLQRRKMKRPSSCTHTMYSIMK 360
 Db 301 RPASIRADVWSFGILLYEMVTLGAPPYVEPPTSIHLQRRKMKRPSSCTHTMYSIMK 360

QY 361 SCWRREADRPSRELRLRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 420
 DB 361 SCWRREADRPSRELRLRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 420
 QY 421 ML 422
 DB 421 ML 422

RESULT 6
 AAY44298
 ID AAY44298 standard; protein; 421 AA.
 XX
 AC AAY44298;
 DT 29-FEB-2000 (first entry)
 XX
 DE Human receptor tyrosine kinase dominant negative mutant-1.
 XX
 KW Human; receptor tyrosine kinase; RTK; tyrosine kinase modulator;
 KW signal transduction tyrosine kinase; tumour; dominant negative mutant;
 KW cancer; adenocarcinoma; RTK associated disorder; adenocarcinoma;
 KW angiogenesis; arthritis; diabetic retinopathy; ischaemic heart disease;
 KW atherosclerosis; inflammation.
 XX
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 146..147
 FT /note= "Wild type Lys at position 147 is deleted"
 XX
 PN WO9964589-A1.
 PD 16-DEC-1999.
 XX
 PF 08-JUN-1999; 99WO-GB001798.
 XX
 PR 11-JUN-1998; 98US-0088959P.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Ghildyal N, Panchamoorthy G;
 XX
 DR WPI; 2000-097538/08.
 XX
 PT New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.
 PT cancers for treating adenocarcinoma.
 XX
 PS Claim 3; Page; 56pp; English.
 CC
 CC The present sequence is a dominant negative mutant of human receptor
 CC tyrosine kinase (RTK), which is obtained by deleting Lys at position 147
 CC of wild type sequence. The mutant modulates biological and/or
 CC pharmacological activity of tyrosine kinase and hence regulates cellular
 CC and tissue physiology. The present sequence is used for treating many
 CC diseases related to or mediated by RTK e.g. adenocarcinomas,
 CC angiogenesis, arthritis, diabetic retinopathy, ischaemic heart disease,
 CC atherosclerosis, inflammation, solid tumours and metastases. Note: The
 CC present sequence is not given in the specification but has been derived
 CC from SEQ ID NO: 3 given in Sequence Listing
 XX
 SQ Sequence 421 AA;

Query Match
 Best Local Similarity 99.3%; Score 2176.5; DB 3; Length 421;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGMTMLLECSLSKLCVIOBQYEVIIIVPTLLVTFILILGVILWLFIREQTOOQSG 60
 DB 1 MGMTMLLECSLSKLCVIOBQYEVIIIVPTLLVTFILILGVILWLFIREQTOOQSG 60

QY 61 PQGIAPVPPRDLUSWEAGHGNVALPLKETSVENFLGATTPALAKLOVPREQLSEVLEQI 120
 DB 61 PQGIAPVPPRDLUSWEAGHGNVALPLKETSVENFLGATTPALAKLOVPREQLSEVLEQI 120
 QY 121 CSGSCGPIFRANNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOPHOYLGHKKNLVL 180
 DB 121 CSGSCGPIFRANNTGDPSPKPSVIL-ALKEPAGLHEVQDFLGRIOPHOYLGHKKNLVL 179
 QY 181 EGCCTEKLPLYMVLEDAVQDGLLGLFWTCRRDVTMDGLLYDLTEKQVHGHKQVLLALE 240
 DB 180 EGCCTEKLPLYMVLEDAVQDGLLGLFWTCRRDVTMDGLLYDLTEKQVHGHKQVLLALE 239
 QY 241 FLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISSTOTIPLKWLAPERLLL 300
 DB 240 FLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISSTOTIPLKWLAPERLLL 299
 QY 301 RPASIRADVWVSFGILLYEMVTLCAPPYEPVPTTSILHLQRRKIMKRPSSCTHTMYSIMK 360
 DB 300 RPASIRADVWVSFGILLYEMVTLCAPPYEPVPTTSILHLQRRKIMKRPSSCTHTMYSIMK 359
 QY 361 SCWRREADRPSRELRLRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 420
 DB 360 SCWRREADRPSRELRLRLLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYS 419
 QY 421 ML 422
 DB 420 ML 421

RESULT 7
 AAB66603
 ID AAB66603 standard; protein; 209 AA.
 XX
 AC AAB66603;
 DT 04-APR-2001 (first entry)
 XX
 DE Human h14833 protein.
 XX
 KW Human; protein kinase; cell growth; tumour; cancer; immune; inflammatory;
 KW respiratory; haematological; bone disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200100879-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US018291.
 XX
 PR 30-JUN-1999; 99US-00345473.
 PR 01-MAY-2000; 2000US-00562480.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Hodge MR, Meyers R, Williamson M;
 XX
 DR WPI; 2001-061977/07.
 XX
 PT New protein kinase polypeptides, nucleic acids and anti-kinase
 PT antibodies, useful for diagnosing and treating e.g. cancer, inflammatory,
 PT immune, cardiovascular and bone disorders.
 XX
 PS Claim 1; Fig 7; 93pp; English.
 XX
 CC The present invention relates to human protein kinase. The proteins are
 CC from new human genes termed h12832, h14138, h14833, h15990, h15993,
 CC h16341 and h2252. The proteins may be used to identify modulators of
 CC their activity. The proteins may also be used to derive products for the
 CC treatment of cellular growth related disorders, malignancies, cancers,
 CC immune, inflammatory, respiratory, haematological and bone-related
 CC disorders
 XX

SQ Sequence 209 AA;
Query Match 49.2%; Score 1079; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.7e-101;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 214 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQKHLPFGDVAARNILMQSDLTAKLCGLGLA 273
DB 1 MTMDGLLYDLTEKQVYHIGKQVLLALEFLQKHLPFGDVAARNILMQSDLTAKLCGLGLA 60
QY 274 YEVYTRGAISSQTITPLKWLAPERLLLRPASIRADVWVSGILLYEMVTLGAPPYEVPPPT 333
DB 61 YEVYTRGAISSQTITPLKWLAPERLLLRPASIRADVWVSGILLYEMVTLGAPPYEVPPPT 120
QY 334 SILEHLQRRKIMKRPSSCTHTMYSMKSCWRREADRSPRELRLRLAEAAIKTADDEAVL 393
DB 121 SILEHLQRRKIMKRPSSCTHTMYSMKSCWRREADRSPRELRLRLAEAAIKTADDEAVL 180
QY 394 QVPELVVPELYAAVAGIRVESLFYNSML 422
DB 181 QVPELVVPELYAAVAGIRVESLFYNSML 209
RESULT 8
ID AAB65707 standard; protein; 183 AA.
XX AAB65707;
XX 27-MAR-2001 (first entry)
DE Novel protein kinase, SEQ ID NO: 236.
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX Mus musculus.
XX WO200073469-A2.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 2000WO-US014842.
XX PR 28-MAY-1999; 99US-0136503P.
XX PA (SUGR-) SUGEN INC.
XX PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
DR WPI; 2001-032161/04.
DR N-PSDB; AAF44736.
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX Claim 10; Fig 1; 310pp; English.
XX The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and

CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
SQ Sequence 183 AA;
Query Match 33.9%; Score 743; DB 4; Length 183;
Best Local Similarity 78.7%; Pred. No. 3.1e-67;
Matches 144; Conservative 17; Mismatches 20; Indels 2; Gaps 1;
QY 242 LOEKHLFGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISS--TOTIPLKWLAPERLL 299
DB 1 LOEKHLFGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISS--TOTIPLKWLAPERLL 60
QY 300 LRPASIRADVWVSGILLYEMVTLGAPPYEVPPPTSIHLQRRKIMKRPSSCTHTMYSTM 359
DB 61 LRPASIRADVWVSGILLYEMVTLGAPPYEVPPPTSIHLQRRKIMKRPSSCTHTMYSTM 120
QY 360 KSCWRREADRSPRELRLRLAEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNY 419
DB 121 KCCWRSEDSRPLLVQLLQRLERASRADDKAVLQVPELVVPELYAAVAGIRVESLFYNY 180
QY 420 SML 422
DB 181 SVL 183
RESULT 9
ID AAE00672 standard; protein; 104 AA.
XX AAE00672;
XX AC AAE00672;
XX DT 02-JUL-2001 (first entry)
XX DE Human protein tyrosine kinase receptor (PTK) from clone HAGHE04.
XX Human; protein tyrosine kinase receptor; PTK; antibacterial; antiviral;
KW antifungal; antiparasitic; sarcoidosis; inflammation; asthma; arthritis;
KW cardiovascular disorder; severe combined immunodeficiency; SCID; vaccine;
KW hyperproliferative disorder; atherosclerosis; brain disorder; leukaemia;
KW multiple sclerosis; Alzheimer's disease; vascular dementia; thrombosis;
KW neurodegenerative disorder; gastrointestinal disorder; cancer; lymphoma;
KW blood coagulation disorder; trauma; cerebrovascular disorder; tendonitis;
KW gene therapy; nephrotic syndrome; glomerulonephritis; allergy; neoplasm;
KW musculo-skeletal disorder; Parkinson's disease; autoimmune disorder;
KW behavioural disorder; renal disorder.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 8..13 /label= Immunogenic_epitope
XX Region 22..33 /label= Immunogenic_epitope
XX Region 43..57 /label= Immunogenic_epitope
XX WO200129564-A1.
XX PD 26-APR-2001.
XX PF 12-OCT-2000; 2000WO-US028066.
XX PR 15-OCT-1999; 99US-0159542P.
XX PR 17-NOV-1999; 99US-0165914P.
XX PR 14-MAR-2000; 2000US-0189027P.
XX PA (HUMA-) HUMAN GENOME SCI INC.

```

XX Ruben SM, Shi Y, Young PE, Ni J;
PI WPI; 2001-290976/30.
XX N-PSDB; AAD03998.
DR New isolated nucleic acid molecule for producing human protein tyrosine
PT kinase receptor.
XX Claim 12; Page 283; 288pp; English.
XX The present sequence is human protein tyrosine kinase receptor (PTK) from
CC clone HAGHE04. The invention relates to human protein tyrosine kinase
CC (PTK) receptors and their corresponding cDNA molecules. PTK receptors are
CC useful in providing immunological probes for differential identification
CC of the tissues or cell types present in a biological sample. PTK is used
CC in methods for the diagnosis, prevention and treatment of various
CC disorders related to PTK such as immune system disorders (severe combined
CC immunodeficiency (SCID), inflammation); hyperproliferative disorders
CC (neoplasm, sarcoidosis); cardiovascular disorders (arrhythmia,
CC atherosclerosis); central nervous system disorders (multiple sclerosis),
CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease);
CC blood coagulation disorders (thrombocytopaenia); autoimmune disorders
CC (biliary cirrhosis, Crohn's disease); respiratory disorders (asthma,
CC allergy); gastrointestinal disorders (inflammatory bowel disease);
CC cerebrovascular disorders (thrombosis, vascular dementia); brain
CC disorders (phenylketonuria); cancers (such as ovarian, lung, bladder,
CC liver, breast and lymphomas); behavioural disorders (Tourette's syndrome)
CC ; musculo-skeletal disorders (arthritis, trauma, tendonitis); renal
CC disorders (nephrotic syndrome, glomerulonephritis); metastases of
CC malignancies and related disorders (leukaemia, multiple myeloma); and
CC infections caused by bacteria, viruses, fungi and parasites. PTK is also
CC useful for screening therapeutic compounds. PTK is used as an antigen in
CC a vaccine to raise an immune response against infectious disease. PTK
CC nucleic acids are useful in gene therapy
XX Sequence 104 AA;
SQ
Query Match 24.7%; Score 542; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.8e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 319 MVTLGAPPYEPVPTTSILEHLQRRKIMKRPSCSTHTMTYIMKSCWRWREADRPSPREURL 378
Db 1 MVTLGAPPYEPVPTTSILEHLQRRKIMKRPSCSTHTMTYIMKSCWRWREADRPSPREURL 60
OY 379 RLEAAIKTADDEAVLQVPVPELYAAVAGIRVESLFYNSML 422
Db 61 RLEAAIKTADDEAVLQVPVPELYAAVAGIRVESLFYNSML 104
RESULT 10
ABB43239
ID ABB43239 standard; peptide; 93 AA.
XX ABB43239;
AC ABB43239;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #10745 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
OS WO200157277-A2.
XX
FN 09-AUG-2001.
XX
PD 30-JAN-2001; 2001WO-US0000669.
XX
PF 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PI

```

```

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human foetal liver.
XX Claim 27; SEQ ID NO 35874; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 93 AA;
SQ
Query Match 20.6%; Score 452; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 6.4e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 64 IAPVPPPPDLWSWAGHGNNVALPLKETSVENFLGATTALAKLQVPRQLSEVLQICSG 123
Db 1 IAPVPPPPDLWSWAGHGNNVALPLKETSVENFLGATTALAKLQVPRQLSEVLQICSG 50
OY 124 SCGPFRAMNTGDPSPKPSVILKALK 150
Db 61 SCGPFRAMNTGDPSPKPSVILKALK 87
RESULT 11
AAM37079
ID AAM37079 standard; protein; 93 AA.
XX AAM37079;
AC AAM37079;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #11116 encoded by probe for measuring placental gene expression.
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX Homo sapiens.
OS WO200157272-A2.
XX
FN 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI

```

```
XX DR WPI; 2001-488897/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
XX PS Claim 27; SEQ ID NO 37348; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP;
XX CC see AA131315-AA157546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders
XX SQ Sequence 93 AA;
XX
Query Match 20.6%; Score 452; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 6.4e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTPALAKIQVPRQLSEVLEQICSG 123
DB 1 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTPALAKIQVPRQLSEVLEQICSG 60
QY 124 SCGPFRANMNTGDPSPKPKSVILKALK 150
DB 61 SCGPFRANMNTGDPSPKPKSVILKALK 87
RESULT 12
AAM76972
ID AAM76972 standard; protein; 93 AA.
AC AAM76972;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 37278.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX Homo sapiens.
XX OS
XX WO200157276-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX 30-JAN-2001; 2001WO-US000668.
XX PF
XX 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 37278; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
```

```
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX SQ Sequence 93 AA;
XX
Query Match 20.6%; Score 452; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 6.4e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTPALAKIQVPRQLSEVLEQICSG 123
DB 1 IAPVPPRDLSEAGHGNNVALPLKETSVENFLGATTPALAKIQVPRQLSEVLEQICSG 60
QY 124 SCGPFRANMNTGDPSPKPKSVILKALK 150
DB 61 SCGPFRANMNTGDPSPKPKSVILKALK 87
RESULT 13
AAM64146
ID AAM64146 standard; protein; 93 AA.
AC AAM64146;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 36251.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
XX OS
XX WO200157275-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX 30-JAN-2001; 2001WO-US000667.
XX PF
XX 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX
XX Example 4; SEQ ID NO 36251; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention
XX SQ Sequence 93 AA;
XX
Query Match 20.6%; Score 452; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 6.4e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Tue Jun 15 09:35:26 2004

Db 433 RIARLSGEGPVLANVSELELPADPKWELSTRITLKGPIGEGCGQVWMAEIGIDKDR 492
QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHKNLVQLEGCCTEKLPVWVLEDV 197
Db 493 TAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTGGGPLYVIVEYA 552
QY 198 AQGDILGFLWTCRRDVTMDGLLY-----DLTEKQVYHIGKOVLLALEFLQEKHL 247
Db 553 AKGNLREEL-RARRP----PGMDYGFDAACRLPEEQLTCKDLVSCAYQVARGMEYLASOKC 607
QY 248 FHGDVAARNILMOSDILAKLGLGLAYEVYTRGATSSQT--IPLKWLAPERLLLRPASI 305
Db 608 IHRDLAARNVLVTEDNVWKIADFGIARDVHNLDDYKKTNGELPVKMWAPALFDRVYTH 667
QY 306 RADVWSFGILLYEMVTLGAP-PYPEVPPTSILEHLQRRKIMKRPSSCTHTMYSIMKSCWR 364
Db 668 QSDVWSFGVLLWEIFTPGGSPVPYGPVBELEFKLLKEGHRMDKPASCCTHDLYMIMRECWH 727
QY 365 WREADRPSPRELRLE--AAIKTADDEAVLOVP 396
Db 728 AVESQRPTEKQOLVEDLDRILTITVTSTDEYLDLSVP 761

Search completed: June 14, 2004, 18:44:17
Job time : 61 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 18:41:39 ; Search time 45 seconds
(without alignments)
2958.860 Million cell updates/sec

Title: US-10-040-884-3
Perfect score: 2192
Sequence: 1 MGMTMLLECSLSKLCVQ.....LYAAVAGIRVESLFYNSML 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2192	100.0	422	4	Q9NSH1	Q9nsH1 homo sapien
2	2183	99.6	422	4	Q9BXV2	Q9bxY2 homo sapien
3	1684.5	76.8	429	11	Q8BZT1	Q8bzt1 mus musculus
4	1357	61.9	340	11	Q8BZH6	Q8bzh6 mus musculus
5	467.5	21.3	828	13	Q9DGK3	Q9dGK3 xenopus lae
6	467.5	21.3	829	13	Q9PSV8	Q9psv8 xenopus lae
7	464.5	21.2	800	13	Q9I8X3	Q9i8X3 brachydanio
8	461	21.0	828	13	Q9I743	Q9i743 xenopus lae
9	459.5	21.0	818	13	Q9I742	Q9i742 xenopus lae
10	459.5	21.0	818	13	Q9PSV9	Q9psv9 xenopus lae
11	455.5	20.8	822	13	Q9I288	Q9i288 pleurodeles
12	453.5	20.7	782	11	Q6I563	Q6i563 mus musculus
13	453.5	20.7	800	11	Q99052	Q99052 mus musculus
14	453.5	20.7	800	11	Q7TSI8	Q7tsi8 mus musculus
15	447	20.4	796	13	Q9I287	Q9i287 pleurodeles
16	445.5	20.3	800	11	Q9JHX9	Q9jhx9 rattus norv

Q8ni15 homo sapien
Q8ni16 homo sapien
Q42127 xenopus lae
Q95ml3 bos taurus
Q800y9 brachydanio
Q90330 coturnix co
Q8C3V5 mus musculus
Q90413 brachydanio
Q86vi4 homo sapien
Q8CIB8 mus musculus
Q8tda0 homo sapien
Q63710 rattus ratt
Q9ttz3 oryctolagus
Q60830 mus musculus
Q60818 mus musculus
Q800z0 brachydanio
Q800z1 brachydanio
Q90z00 brachydanio
Q63827 rattus norv
Q9qvv7 rattus sp.
Q63711 rattus ratt
Q8ixc7 homo sapien
Q8cfk8 mus musculus
Q80t10 mus musculus
Q8cim9 mus musculus
Q9tt07 canis fami1
Q96ke5 homo sapien
Q721l9 aplysia cal
Q8n685 homo sapien

ALIGNMENTS

RESULT 1

Q9NSH1 PRELIMINARY; PRT; 422 AA.
ID Q9NSH1
AC Q9NSH1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP761P1010.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amnygdala;
RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353940; CAB89250.1; --
DR PIR; T48680; T48680.
DR HSSP; P08631; 1AD5.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Hypothetical protein; ATP-binding; Kinase; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 422 AA; 47546 MW; B7CD8BC006029D3B CRC64;
Query Match 100.0%; Score 2192; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.9e-186;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTRMLLECSLSDKLCVIOEQKQYEVIIPTLLVTIFILLGVILWLFIREORTQOQSG 60
 DB |||||
 QY 1 MGTRMLLECSLSDKLCVIOEQKQYEVIIPTLLVTIFILLGVILWLFIREORTQOQSG 60
 DB |||||
 QY 61 PQGIAPVPPRDLWEAGHGGNVALPLKETSVENFLGATTTPALAKLOVPREQLSEVLQI 120
 DB |||||
 QY 61 PQGIAPVPPRDLWEAGHGGNVALPLKETSVENFLGATTTPALAKLOVPREQLSEVLQI 120
 DB |||||
 QY 121 CSGSGCPIFRANMNTGDPKPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHKNLVOL 180
 DB |||||
 QY 121 CSGSGCPIFRANMNTGDPKPSVILKALKEPAGLHEVQDFLGRIOFHQYLGKHKNLVOL 180
 DB |||||
 QY 181 EGCCTEKLPLYMVLDEVAQDGLLGFMTCCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 DB |||||
 QY 181 EGCCTEKLPLYMVLDEVAQDGLLGFMTCCRRDVTMDGLLYDLTEKQVYHIGKQVLLALE 240
 DB |||||
 QY 241 FLOEKHLFGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISSSTQTIPLKWLAPERLLL 300
 DB |||||
 QY 241 FLOEKHLFGDVAARNILMQSDLTAKLCGLGLAYEYVTRGAISSSTQTIPLKWLAPERLLL 300
 DB |||||
 QY 301 REASIRADVWSFGILLYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPPSSCTHTWYSIMK 360
 DB |||||
 QY 301 REASIRADVWSFGILLYEMVTLGAPPYEVPPPTSILEHLQRRKIMKRPPSSCTHTWYSIMK 360
 DB |||||
 QY 361 SCWRWEADRPSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420
 DB |||||
 QY 361 SCWRWEADRPSPRELRLRLAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNS 420
 DB |||||
 QY 421 ML 422
 DB |||||
 QY 421 ML 422
 DB |||||

RESULT 2

Q9BX2 PRELIMINARY; PRT; 422 AA.

AC Q9BX2; (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FGF receptor 4b.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,
 Tang R., Chen X., Wu C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF251059; AAK34949.1; -;
 DR HSSP; P08631; IAD5.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; P00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR ATP-binding; Kinase; Receptor; Tyrosinase; Tyrosine-protein kinase.
 KW SEQUENCE 422 AA; 47583 MW; 81D1F676D6F2E26 CRC64;

Query Match 99.6%; Score 2183; DB 4; Length 422;
 Best Local Similarity 99.5%; Pred. NO. 1.2e-185;
 Matches 420; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 3

Q8BZT1 PRELIMINARY; PRT; 429 AA.

AC Q8BZT1; (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to FGF receptor 4b.
 GN AI326477.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=22354683; PubMed=12456851;
 RA The PANTOM Consortium,
 the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK036066; BAC28386.1; -;
 DR MGD; MGI:2141396; AI326477.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; P00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.


```
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 828 AA; 93211 MW; 72E2052635D5E323 CRC64;

Query Match 21.3%; Score 467.5; DB 13; Length 828;
Best Local Similarity 30.1%; Pred. No. 1.3e-32;
Matches 122; Conservative 84; Mismatches 162; Indels 37; Gaps 14;

QY 21 EKQYEVIIVPTLLVITFL-ILGLVILWLFIREQ--RTQQRSGP--QGIAPVPPRDLNW 75
DB 386 ESRYMIIIT---SGFLAVAMAIVILCRMQTPHKSQTLOTPTVHKLAKFLIRQFSL 442
QY 76 EAGHGNGVALPL-KETSVENFLGATTPAL-----AKLOVPREOLSEVL-EQICSGSC 125
DB 443 ESSSSKSSAPLIRITRLSSCAPMLPGVMEVELPLDAKWEFPRDL--VLGKPLGEGCF 500
QY 126 GPIFRA---NMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRITQFHYLGKHNVLQLEG 182
DB 501 GQVRAEGYGIKDRPEKPVTVAVKMLKONGTGDLSLISELMKVIKHNIIINLLG 560
QY 183 CTEKPLPLYMVLVDVAGDLGLFWTCRRDVTMDGLLYDLTE-----KQVYHIGKQ 234
DB 561 VCTQEGFLFVVEYASKGNLREFL-RARRPTPEDA--FDITKVPBELLSEFKDLVSCAYQ 617
QY 235 VLLALGFLOKHLFHGDVAARNILMOSDLTAKLCGLGLAVEYVTRGAISSTQT--IPLKW 292
DB 618 VARGMEYLESKRCIHRDLAARNVLVAEDNVKMTADFLARGVHDIDYKKTSGRLPVKW 677
QY 293 LAPERILLRPASIRADVWSFGILLYEMVTILGAPPYPEVPTTSILEHLQRRKIMKRPSST 352
DB 678 MAPEALFDRVYTHQSDIWSFGVLTWELFTLGSGPYGIPVEELFKLLREGHRMDKPSNCT 737
QY 353 HTMYSIMKSWRWEADRPSPRELRLLEAAIKTADDEAV-LQVP 396
DB 738 HELYMLMRECWHAVPTQRTPFKQLVEHLDRILTAVSEYDLDSMP 782

RESULT 6
Q9PSV8 PRELIMINARY; PRT; 829 AA.
AC Q9PSV8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FGF receptor 4b.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongo I., Kengaku M., Okamoto H.;
RT "Differential employment of FGF signaling system for the embryonic
induction."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB007037; BAA22282.1; -.
DR PIR; JC4583; JC4583.
DR HSP; P11362; IFCK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 829 AA; 93332 MW; 47463466399BF571 CRC64;

Query Match 21.3%; Score 467.5; DB 13; Length 829;
Best Local Similarity 30.1%; Pred. No. 1.3e-32;
Matches 122; Conservative 84; Mismatches 162; Indels 37; Gaps 14;

QY 21 EKQYEVIIVPTLLVITFL-ILGLVILWLFIREQ--RTQQRSGP--QGIAPVPPRDLNW 75
DB 387 ESRYMIIIT---SGFLAVAMAIVILCRMQTPHKSQTLOTPTVHKLAKFLIRQFSL 443
QY 76 EAGHGNGVALPL-KETSVENFLGATTPAL-----AKLOVPREOLSEVL-EQICSGSC 125
DB 444 ESSSSKSSAPLIRITRLSSCAPMLPGVMEVELPLDAKWEFPRDL--VLGKPLGEGCF 501
QY 126 GPIFRA---NMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRITQFHYLGKHNVLQLEG 182
DB 502 GQVRAEGYGIKDRPEKPVTVAVKMLKONGTGDLSLISELMKVIKHNIIINLLG 561
QY 183 CTEKPLPLYMVLVDVAGDLGLFWTCRRDVTMDGLLYDLTE-----KQVYHIGKQ 234
DB 562 VCTQEGFLFVVEYASKGNLREFL-RARRPTPEDA--FDITKVPBELLSEFKDLVSCAYQ 618
QY 235 VLLALGFLOKHLFHGDVAARNILMOSDLTAKLCGLGLAVEYVTRGAISSTQT--IPLKW 292
DB 619 VARGMEYLESKRCIHRDLAARNVLVAEDNVKMTADFLARGVHDIDYKKTSGRLPVKW 678
QY 293 LAPERILLRPASIRADVWSFGILLYEMVTILGAPPYPEVPTTSILEHLQRRKIMKRPSST 352
DB 679 MAPEALFDRVYTHQSDIWSFGVLTWELFTLGSGPYGIPVEELFKLLREGHRMDKPSNCT 738
QY 353 HTMYSIMKSWRWEADRPSPRELRLLEAAIKTADDEAV-LQVP 396
DB 739 HELYMLMRECWHAVPTQRTPFKQLVEHLDRILTAVSEYDLDSMP 783

RESULT 7
Q918X3 PRELIMINARY; PRT; 800 AA.
AC Q918X3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 3.
GN FGFR3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
```

```

OX NCBI_TaxID=7955;
RN SEQUENCE FROM N.A.
RX MEDLINE=21184119; PubMed=11287195;
RA Sleptsova-Friedrich I., Li Y., Emelyanov A., Ekter M., Korzh V.,
RT Ge R.;
RL "fgfr3 and regionalization of anterior neural tube in zebrafish.";
MEch. Dev. 102:213-217(2001).
DR HSSP; P11362; 1FGK.
DR ZFIN; ZDB-GENE-000816-1; fgfr3.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 800 AA; 89716 MW; 8092DC0272A5BAD1 CRC64;

Query Match      21.2%; Score 464.5; DB 13; Length 800;
Best Local Similarity 29.2%; Pred. No. 2.3e-32;
Matches 119; Conservative 84; Mismatches 164; Indels 41; Gaps 11;

QY 20 QEQYEVIIVTLLVTFILLLGVI-----LMLFIREQRTQOORSGP--QGAPVPPPRDL 73
Db 357 REDDYADILLYVTSVLFILTWIIILCRMWI-----NTQKTLPAFPVQKLSKPLKQV 411
QY 74 SWEAGHGNGVALPL-KETSVENFLGATTPALAKLOVPE-----QLSEVLEQICS 122
Db 412 SLENSNSMNTPLVRIARLSSDGMPLPNVSELELSPDKWEFTRTKLTLGKPLGEGCF 471
QY 123 GSCGPIFRANMNTGDPSPKSVILKALKEPAGLHEVQDFLGRIOHQVYLGKHNVLQLEG 182
Db 472 GOVMAEAGIDKEKPKNLTVAKMLKDDGTDKDLSLSEMEMMMKMGKHKNIINLLG 531
QY 183 CTTEKFLYVLEDAVQGDLLGLFWTCRRDVMVTMDGLLYD-----LTEXQVYHIG 232
Db 532 ACTQDGLYVLEAYASKNRLREYL-RARRP-----PGMDYSDTCCKIPNEILTFKDIUSCA 586
QY 233 KQVLLALEFLQEKHLFGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTOT--IPL 290
Db 587 YQVARGMEYLASKKCIHRDPAARNVLTEDNVNMIADFGLDARVDHNDIYKKTNGSLPV 646
QY 291 KWLAPERLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPTPTILEHLQRRKMKPSS 350
Db 647 KWAPEALFDRVYTHQSDVMSYGVLLWEITLGGSPYPGIPVEELFKLLKEGHRMDKPN 706
QY 351 CTHWTMSKWRREADRPSRELRLRLAEAIK-TADDEAV-LQVP 396
Db 707 CTHELYMIMRECWAHPVQRPFTQLVEDHDLVLSMTSTDEYLDLSVP 754

RESULT 8
Q91743 ID Q91743 PRELIMINARY; PRT; 828 AA.
AC Q91743;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```

```

DE FGF receptor 4 precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RX MEDLINE=96136300; PubMed=8573131;
RA Riou J.F., Clavilier L., Boucaut J.C.;
RT "Early regionalized expression of a novel Xenopus Fibroblast Growth
RT factor receptor in Neuroepithelium.";
RL Biochem. Biophys. Res. Commun. 218:198-204(1996).
DR EMBL; X89807; CAAG1930.1; -.
DR FIR; JC4583; JC4583.
DR HSSP; P11362; 1FGK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal;
KW Transferase; Tyrosine-protein kinase.
FT SIGNAL 1 38 POTENTIAL.
SQ SEQUENCE 828 AA; 93417 MW; 089EB0D887603524 CRC64;

Query Match      21.0%; Score 461; DB 13; Length 828;
Best Local Similarity 29.4%; Pred. No. 4.9e-32;
Matches 118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;

QY 21 EKQYEVIIVPT--LLVTIFILLLGVIILFWLFIREFQRTQOORSGPQGIAPVPPRDLSEAG 78
Db 387 ESRVMDIIIVTSGFLAVAMAIMVILCEMQTPHKSQTLPQTVHKLAKFLIIRQFSLESS 446
QY 79 HGNVALPL-KETSVENFLGATTPAL-----AKLQVPREQLSEVL-EQICSGSGCPI 128
Db 447 SSKSSAPLIRITLSSSCAPMLPGVMEVELDLDAKWEFFRDL--VLGKPLGEGCGV 504
QY 129 FRA---NMNTGDSKPKSVILKALKEPAGLHEVQDFLGRIOHQVYLGKHNVLQLEGCCCT 185
Db 505 VRAEGVIEKDRKPKVTVAVKMLKONGTDKDLSELMKVIKHKNIINLLGVCT 564
QY 186 EKPLVMVLEDAVQGDLLGLFWTCRRDVMVTMDGLLYDLTE-----KQVYHIGQVLL 237
Db 565 QEGFLFVIVEYASKNRLREYL-RARRPPTPEDA--FDITKVPPEELSFKDLVSCAVQVAR 621
QY 238 ALFELQEKHLFGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTOT--IPLKWLAP 295
Db 622 GMEYLESKRCIHRDLAARNVLAEDNVNMIADFGLDARVDHNDIYKKTNGSLPVKMAP 681
QY 296 ERLLRPASIRADVMSFGILLYEMVTLGAPPYVEVPTPTILEHLQRRKMKRPSSTHTM 355
Db 682 EALFDRVYTHQSDVMSYGVLLWEITLGGSPYPGIPVEELFKLLKEGHRMDKPSNCTHEL 741
QY 356 YSIMKSKWRREADRPSRELRLRLAEAIK-TADDEAV-LQVP 396
Db 742 YMLRECWAHPVQRPFTQLVLEHLDRILTAVSEYLDLSMP 782

```

296 ERLLRPASIRADVMSFGILLYEMVTLGAPPYEPVPTTSILEHLQRRKIMRPSCHTMM 355
671 EALFDVRYTHQSDIWSFGVLTFEFTLGGSPYGPVPEELFKLLRGRHMDKPSNCTHEL 730
356 YSIMKSCWRREADRPSRELRLRLLEAAIKTADDEAV-LQVP 396
731 YMLRECWHAVPSQRPFTKQLVEQLDRILTAVSEYLDLSMP 772
RESULT 10
Q9PSV9 PRELIMINARY; PRT; 818 AA.
AC Q9PSV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FGF receptor 4a.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongo I., Kengaku M., Okamoto H.;
RT "Differential employment of FGF signaling system for the embryonic induction";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB007036; BAA22849.1; -.
DR HSP; F11362; lFGK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 3.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
FT SIGNAL 1 26 POTENTIAL.
SQ SEQUENCE 818 AA; 92067 MW; A8CBA4341C9230C1 CRC64;

Query Match 21.0%; Score 459.5; DB 13; Length 818;
Best Local Similarity 29.4%; Pred. No. 6.6e-32;
Matches 118; Conservative 83; Mismatches 170; Indels 31; Gaps 11;
QY 21 EKYEVITVPT--LLVTIFLLGLVILWLFIREORTQQRSGQGIAVPPPPRDLSEAG 78
DB 376 ESRMDIITTSGLAVMAIVILCRMOTPHSKQTLPAPVHKLAKFLFIQFSLESS 435
QY 79 HGNVNLPL-KETSVENFLGATTPAL-----AKLQVPREQLSEVL-EQICSGSGCPI 128
DB 436 SSGKSSAPLIRITLSSSCAPMLPGVMEVELPLDAKWEFPRDL--VLGKPLGEGCGQV 493
QY 129 FRA---NMWTDGSKPKSVILKALKEPAGLHVQDFLGRIOFHQYLGKHNVLQEGCCT 185
DB 494 VRAEGYIEKDRPEKPTVAVKMLKNGTQDKDLSLISELMELMKVIGKHNNIINLLGVST 553
QY 186 EKPLYMVLVEDVAGDLGLFWTCRRDVTMDGLLYDLTE-----KQYHIGKQVLL 237
DB 554 QEGFLFVIVEYASKNLREFL-RARRPTPEDA--FDITKPEDLSFKDLVSCAYQVAR 610
QY 238 ALEFLQPKHLPHGDAARNILMQSDLTAKLGLGLAYEVYTRGAISSQT--IPLKWLAP 295
DB 611 GMEYLESKRCIHRDLAARNVLVAEDNVNMKIADFLARGVHDIDYIKKTSNGRLPVKWPAP 670

RESULT 9
Q91742 PRELIMINARY; PRT; 818 AA.
AC Q91742;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor-4 precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95137391; PubMed=7835703;
RA Shiozaki C., Tashiro K., Asano-Miyoshi M., Saigo K., Emori Y.,
RA Shiozaki K.;
RT "Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor-4 of Xenopus laevis";
RL Gene 152:215-219 (1995).
DR EMBL; D31761; BAA06539.1; -.
DR PIR; JC4058; JC4058.
DR HSP; F11362; lFGK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal;
KW Transferase; Tyrosine-protein kinase.
FT SIGNAL 1 26 POTENTIAL.
SQ SEQUENCE 818 AA; 92065 MW; AB741A59E8410E41 CRC64;

```
Db 554 QGGLFVIVEYASKGNLREFL-RARRPPTPEDA--FDITKVPDELLSKDLVSCAYQVAR 610
QY 238 ALFFLOEKHLFHGDVAARNILMQSDLTAKLCLGLAYEVYTRGAISSTQT--IPLKWLAP 295
Db 611 GMEYLSKRCIHRDLAARNVLVAEDNVUMKIADFGLAGVHDIDYKKTNSGRULPVKWMAP 670
QY 296 ERLLRPASIRADVWFGILLYEMVTGLAPPYEPVPTSLILEHLQRRKIMKRPSSCTHTM 355
Db 671 EALFDVRYTHQSDIMSEFGVLTWEIFTLGSGSPYGPVPEELFKLLRGHRMDKPSNCTHEL 730
QY 356 YSIMKSCWRREADRSPRELRLRLAEAAIKTADDEAV-IQVP 396
Db 731 YMLMRECWAHPVSQRPFTFKQLVEQLDRILTAIVSEYLDLSMP 772

RESULT 11
Q91288
ID Q91288 PRELIMINARY; PRT; 822 AA.
AC Q91288;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor.
OS Pleurodeles waltlii (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Pleurodeles.
OX NCBI_TaxID=8319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93130775; PubMed=1483392;
RA Shi D.L., Feige J.J., Ricou J.F., Desimone D.W., BoucAUT J.C.;
RT "Differential expression and regulation of two distinct fibroblast
RT growth factor receptors during early development of the urodele
RT amphibian Pleurodeles waltlii";
RL Development 116:261-273(1992).
DR EMBL; X65059; CAA46192.1; -.
DR FIR; B49151; B49151.
DR PIR; S19947; S19947.
DR HSP; P11362; IFGK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00047; Ig; 3.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
SQ Tyrosine-protein kinase.
SEQUENCE 822 AA; 92068 MW; 3EC4BA4B9C9AB81A CRC64;

Query Match 20.8%; Score 455.5; DB 13; Length 822;
Best Local Similarity 29.2%; Pred. No. 1.5e-31;
Matches 118; Conservative 82; Mismatches 169; Indels 35; Gaps 11;

QY 21 EKQYEIVTPT--LLVTFILLLGVILWLFREORTQOGRSGPGIAVPVPPDLSEAG 78
Db 383 ETRYDIIIVTSGSLALLMAVIVVCLRMQLPPTKTHLEPVAHVKLFRFFLMROFLESS 442
QY 79 HGGNVALPLKETSVENFIGATTPAL-----AKLQVFEQLSEVL-EQICSGSG 126
```

```
Db 443 SSGKSTSL--VRVITLSSCTPMLEGVLEFDLPLDSKWEFFPRERL--VLGKPLGSGCFG 498
QY 127 PIFRA---NMNTGDPSPKPSVILKALKEPAGLHEVQDFLGRIOFHQVYLGKHKHNLVQLEG 183
Db 499 QVRAEAYGINKDQDPDKAITVAIKIVKDKGTDKELSDLSISELMELKMGKHKNIINLGV 558
QY 184 CTEKIPLYNVLEDVAGDILLGLFWTCRRDVTMDGLLYDLTE-----KQVYHTGKQV 235
Db 559 CTQDGLYIMVEYASKGNLREFL-RARRP--PSPDYTFDMTKVPKPEQLSFQDLVSCSYQV 615
QY 236 LLALEFLOEKHLFHGDVAARNILMQSDLTAKLCLGLAYEVYTRGAISSTQT--IPLKWL 293
Db 616 ARGMAYLESKRCIHRDLAARNVLVAEDNVUMKIADFGLAGVHDIDYKKTNSGRULPVKWM 675
QY 294 APERLLRPASIRADVWFGILLYEMVTGLAPPYEPVPTSLILEHLQRRKIMKRPSSCTHT 353
Db 676 APEALFDVRYTHQSDIMSEFGVLTWEIFTLGSGSPYGPVPEELFKLLRGHRMDKPSNCTH 735
QY 354 TMSYIMKSCWRREADRSPRELRLRLAEAAIKTADDEAV-IQVP 396
Db 736 ELYMLMRECWAHPVSQRPFTFKQLVEQLDRILTAIVSEYLDLSMP 779

RESULT 12
Q61563
ID Q61563 PRELIMINARY; PRT; 782 AA.
AC Q61563;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 3, acid box-deleted isoform.
GN FGFR3 OR FR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimizu A., Seo M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE OF 224-346 FROM N.A.
RX MEDLINE=94209351; PubMed=7512569;
RA Chellatah A.T., McEwen D.G., Werner S., Xu J., Ornitz D.M.;
RT "Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in
RT immunoglobulin-like domain III creates a receptor highly specific for
RT acidic FGF/FGF-1.";
RT J. Biol. Chem. 269:11620-11627(1994).
DR EMBL; AF024638; AAB81604.1; -.
DR HSP; L26492; AAK21491.2; -.
DR MGD; MGI:95524; Fgfr3.
DR GO; GO:0045597; P:positive regulation of cell differentiation; IMP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR004074; Ili_receptor1/II.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01536; INTRLNIR12F.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Transferase;
SQ Tyrosine-protein kinase.
```

SQ SEQUENCE 782 AA; 85871 MW; 90262B44P0CFB49B CRC64;

Query Match 20.7%; Score 453.5; DB 11; Length 782;
 Best Local Similarity 30.5%; Pred. No. 2.1e-31;
 Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFILLLGVILWLFIREQRTQOQRSGPGQIAPV---PPRDLSSWEAGHGNNVALPLKET 90
 DB 357 VVFELFILVVAAILCRLRSPPKGLGSPVHKVSRFPLKRVLSLSSNMSNTPL--V 414

QY 91 SVENFLGATTAPALA---KLQVP-----REQLSVEVLQICSGSCGPIFRANNTGD 137
 DB 415 RIARLSSGGPGVLANVSELELPADPKWLSRTRLTGLKPLGEGCFQGVVMAEAGIDKDR 474

QY 138 PPKPKSVILKALKEPAGLHEVDFLGRIOFHQVLGKHKNLVQLEGCCTEKPLPLYMVLEDV 197
 DB 475 TAKPVTVAVMKLDKDATDSDLVSEMEMMKWIGKHKNIIINLLGACTGGPLVYLVEYA 534

QY 198 AQGDLLGLFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHL 247
 DB 535 AKGNLREFL-RARRP-----PGMDYSPDACRLPEEQLTCKDLVSCAYQVARGMEYLASQKC 589

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWLAPERILLRPASI 305
 DB 590 IHRDLAARNVLTEDNVMKIADPGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTH 649

QY 306 RADVWSFGILLYEMVTLGAPPYEVPTSTLHQLQRKIMKRPSSCTHTMYSIMKSCWRW 365
 DB 650 QSDVWSFGVLLWEIFLTGSPYGPVVEELFKLLKGHRMDKDPASCTHLYLMIMRECWA 709

QY 366 READRPSRELRLRLE--AAIKTADDEAVLQVP 396
 DB 710 VPSQRTFQQLVEDLDRILLTVTSTDEYLDLSPV 742

RESULT 13

Q99052 ID Q99052 PRELIMINARY; PRT; 800 AA.

AC Q99052; 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fibroblast growth factor receptor.
 GN FGFR3 OR FLG-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=91296390; PubMed=1648703;
 RA Avivi A., Zimmer Y., Yaron A., Yarden Y., Givol D.;
 RT "Fig-2, a new member of the family of fibroblast growth factor
 RT receptors [published erratum appears in Oncogene 1992 Apr;7(4):823].";
 RL Oncogene 6:1089-1092 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Avivi A., Zimmer Y., Yaron A., Yarden Y., Givol D.;
 RT "Errata: lg-2, a new member of the family of fibroblast growth factor
 RT receptor.";
 RL Oncogene 7:823-823 (1992).
 DR ENBL; X58255; GAA41209.1; --
 DR HSSP; P11362; IFGK.
 DR MGD; MGI:95524; Fgfr3.
 DR GO; GO:0045597; P:positive regulation of cell differentiation; IMP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG c2.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR001245; Tyr. kinase.
 DR InterPro; IPR008266; Tyr. kinase_AS.
 DR Pfam; PF00047; Ig; 3.

DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot. Kinase; 1.
 DR SMART; SM00408; IGC2; 3
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS50835; IG LIKE; 3.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal;
 KW Transferase; Tyrosine-protein kinase.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 800 FIBROBLAST GROWTH FACTOR RECEPTOR.
 SQ SEQUENCE 800 AA; 87691 MW; B376D47DBE8B312 CRC64;

Query Match 20.7%; Score 453.5; DB 11; Length 800;
 Best Local Similarity 30.5%; Pred. No. 2.2e-31;
 Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFILLLGVILWLFIREQRTQOQRSGPGQIAPV---PPRDLSSWEAGHGNNVALPLKET 90
 DB 375 VVFELFILVVAAILCRLRSPPKGLGSPVHKVSRFPLKRVLSLSSNMSNTPL--V 432

QY 91 SVENFLGATTAPALA---KLQVP-----REQLSVEVLQICSGSCGPIFRANNTGD 137
 DB 433 RIARLSSGGPGVLANVSELELPADPKWLSRTRLTGLKPLGEGCFQGVVMAEAGIDKDR 492

QY 138 PPKPKSVILKALKEPAGLHEVDFLGRIOFHQVLGKHKNLVQLEGCCTEKPLPLYMVLEDV 197
 DB 493 TAKPVTVAVMKLDKDATDSDLVSEMEMMKWIGKHKNIIINLLGACTGGPLVYLVEYA 552

QY 198 AQGDLLGLFWTCRRDVTMTDGLLY-----DLTEKQVYHIGKQVLLALEFLQEKHL 247
 DB 553 AKGNLREFL-RARRP-----PGMDYSPDACRLPEEQLTCKDLVSCAYQVARGMEYLASQKC 607

QY 248 FHGDVAARNILMQSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKWLAPERILLRPASI 305
 DB 608 IHRDLAARNVLTEDNVMKIADPGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTH 667

QY 306 RADVWSFGILLYEMVTLGAPPYEVPTSTLHQLQRKIMKRPSSCTHTMYSIMKSCWRW 365
 DB 668 QSDVWSFGVLLWEIFLTGSPYGPVVEELFKLLKGHRMDKDPASCTHLYLMIMRECWA 727

QY 366 READRPSRELRLRLE--AAIKTADDEAVLQVP 396
 DB 728 VPSQRTFQQLVEDLDRILLTVTSTDEYLDLSPV 760

RESULT 14

Q99052 ID Q99052 PRELIMINARY; PRT; 800 AA.

AC Q99052; 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fgfr3 protein.
 DE Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,


```
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.
RA Rahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
SQ EMBL; BC053056; AAH53056.1; -.
SEQUENCE 800 AA; 87676 MW; 2A7215F13F67E5E9 CRC64;

Query Match      20.7%; Score 453.5; DB 11; Length 800;
Best Local Similarity 30.5%; Pred. No. 2.2e-31;
Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;

QY 34 VTIFLLGLVILWFIREQRTQOQSGPQGIAPV---PPPRDLSEAGHGNNVALPLKET 90
Db 375 VVFFFLVVAAILCLRSPPKGLGSPVHKVSRFPFLKRVLSLESSNMSNTPL--V 432
QY 91 SVENFLGATTPALA---KLQVP-----REQLSEVLEQICSGCGPIFRANMNTGD 137
Db 433 RTARLSSGSGPVLNAVSELELPADPKWELSRSLTLGKPLGEGCFQGVMAEAIGDKDR 492
QY 138 PSKPKSVILKALKEPAGLHEVQDFLGRIQPHOYLGHKHNVLQLEGCTEKLPLYMVLVDV 197
Db 493 TAKPTVAVKMLKDDATDKDLSLVSEMEMMKMGKHNIINLLGACTQGGPLYVLVEYA 552
QY 198 AQGDLGLFWTCRDVMTWMDGLLY-----DLTEKQVYHIGKVLLAEFLQEKHL 247
Db 553 AKGNLREFL--RARRP----PGMDYSFDACRLPEQLTKDLVSCAYQVARGMEYLASQKC 607
QY 248 FHGDDVAARNILMOSDLTAKLGLGLAYEVYVTRGAISTQT--IPLKWLAPERLLLRPAS 305
Db 608 IHRDLAARNVLTEDNNMKIADFGIARVNDLYKKTTNGRLPVKWMAPALFDRVYTH 667
QY 306 RADVWSFGILLVEMVTLGAPPYVEVPPTSILEHLQRRKMKRPSCTHTMYSIMKSCWRW 365
Db 668 QSDVWSFGVLLWEIFTLGGSPYGPVPEELFKLLKEGHRMDKPCACTHLYLMIMRECWEA 727
QY 366 READRPSRELRLRL--AAIKTADAEAVLQVP 396
Db 728 VPSQRPTFKQLVEDLDRILVTSTDEYLDLSPV 760

RESULT 15
Q91287 PRELIMINARY; PRT; 796 AA.
AC Q91287;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor receptor 3.
OS Pleurodeles waltlii (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Pleurodeles
NCBI_TaxID=8319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94299014; PubMed=8026621;
RA Shi D.L., Launay C., Fromentoux V., Feige J.J., Boucaut J.C.;
RT "Expression of fibroblast growth factor receptor-2 splice variants is
RT developmentally and tissue-specifically regulated in the amphibian
RT embryo.";
RL Dev. Biol. 164:173-182(1994).
```

```
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94274759; PubMed=8006062;
RA Shi D.L., Fromentoux V., Launay C., Unbhauser M., Boucaut J.C.;
RT "Isolation and developmental expression of the amphibian homolog of
RT the fibroblast growth factor receptor 3.";
RL J. Cell Sci. 107:417-425(1994).
DR EMBL; X75603; CAAS3271.1; -.
DR FIR; S38579; S38579.
DR HSSP; P11362; IFGK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; ig; 3.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE D; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 796 AA; 88288 MW; 226D99A0B6D1D92D CRC64;

Query Match      20.4%; Score 447; DB 13; Length 796;
Best Local Similarity 28.8%; Pred. No. 8.2e-31;
Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;

QY 33 LVTFILLGLVILWFIREQRTQOQSGPQGIAPVPPPRDLSEAGHGNNVALPL-KETS 91
Db 368 VAVVILVVIITTYKMKPSKKTMTATVHKVSKFPLKRVLSLESSNMSNTPLVRITR 427
QY 92 VENFLGATTPALAKLQVP-----REQLSEVLEQICSGCGPIFRANMNTGDPSPK 141
Db 428 LSSDGPMLNAVSELELPADPKWELSRSLTLGKPLGEGCFQGVWADAVGTEKDPNKA 487
QY 142 KSVILKALKEPAGLHEVQDFLGRIQPHOYLGHKHNVLQLEGCTEKLPLYMVLVDY 201
Db 488 TSVAVKMLKDDATDKDLSLVSEMEMMKMGKHNIINLLGACTQGGPLYVLVEYASKG 547
QY 202 LLGFLWTCRDVMTWMDGLLY-----DLTEKQVYHIGKVLLAEFLQEKHLFHGD 251
Db 548 LREYL--RARRP----PGMDYSFDTKLPEEQITFKDLVSCAYQVARGMEYLASQKCIHRD 602
QY 252 VAARNILMOSDLTAKLGLGLAYEVYVTRGAISTQT--IPLKWLAPERLLLRPASIRADV 309
Db 603 LAARNVLTEDNNMKIADFGIARVNDLYKKTTNGRLPVKWMAPALFDRVYTHQSDV 662
QY 310 WSFGILLVEMVTLGAPPYVEVPPTSILEHLQRRKMKRPSCTHTMYSIMKSCWRW 369
Db 663 WSFGVLLWEIFTLGGSPYGPVPEELFKLLKEGHRMDKPCACTHLYLMIMRECWEA 722
QY 370 RSPRELRLRL--AAIKTADAEAV-LQVP 396
Db 723 RPTFKQLVEDLDRILVTSTDEYLDLSPV 751

Search completed: June 14, 2004, 18:45:44
Job time : 46 secs
```

This Page Blank (uspto)